(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
7 December 2006 (07.12.2006)

PCT

(10) International Publication Number
WO 2006/130328 A2

(51) International Patent Classification: Not classified

(21) International Application Number:
PCT/US2006/018411

(22) International Filing Date: 12 May 2006 (12.05.2006)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

60/680,479	13 May 2005 (13.05.2005)	US
60/740,291	29 November 2005 (29.11.2005)	US

(71) Applicant *(for all designated States except US)*: **NOVARTIS VACCINES AND DIAGNOSTICS, INC.** [US/US]; 4560 Horton Street, Emeryville, CA 94608 (US).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **SORIANI, Marco** [IT/IT]; Via Fiorentina, 1, I-53100 Siena (IT). **SANTI, Isabella** [IT/IT]; Via Fiorentina, 1, I-53100 Siena (IT).

(74) Common Representative: **NOVARTIS VACCINES AND DIAGNOSTICS, INC.**; 4560 Horton Street, Emeryville, CA 94608 (US).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, LY, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 2006/130328 A2

(54) Title: SERUM RESISTANCE FACTORS OF GRAM POSITIVE BACTERIA

(57) Abstract: A newly identified serum resistance factor of gram positive bacteria can be used to treat or prevent bacterial infection.

SERUM RESISTANCE FACTORS OF GRAM POSITIVE BACTERIA

[01] This application claims the benefit of and incorporates by reference co-pending provisional applications Serial No. 60/680,479 filed May 13, 2005 and Serial No. 60/740,291 filed November 29, 2005.

FIELD OF THE INVENTION

[02] This invention is in the fields of immunology and vaccinology. In particular, it relates to a newly identified serum resistance factor of gram positive bacteria and its use in compositions for the treatment and prevention of bacterial infection.

BACKGROUND OF THE INVENTION

[03] The gram positive bacteria Group B *Streptococcus* (GBS) is one of the most important causes of life-threatening bacterial infection in newborn infants, pregnant women, the elderly and individuals with chronic illness. Other gram positive bacteria such as *Streptococcus pyogenes* (GBS), *Streptococcus pneumoniae* (Strep pneumo), and *Staphylococcus aureus* (Staph) are also implicated in significant morbidity and mortality worldwide.

[04] Various streptococci express on their surface multifunctional proteins that mediate both bacterial adhesion and acquisition of immune system components, contributing to a successful colonization of host mucosal surfaces (Jarva *et al.*, 2003; Talay, 2005). In particular, *Streptococcus agalactiae* (GBS) and *Streptococcus pyogenes* (GAS) express a number of functionally-related proteins, characterized by their capacity to bind both human immunoglobulins (Boyle, 1998) and fluid-phase complement regulators (Jarva *et al.*, 2004; Lindahl *et al.*, 2005). In GBS, receptors for IgA and/or IgG belong to the M protein family (Stenberg *et al.*, 1992); M proteins interact with the type II Fc region of immunoglobulins outside their antigen-combining site (Cunningham, 2000).

[05] In GBS, the Bac protein (beta antigen) binds with high affinity to the Fc part of human serum IgA (Bevanger, 1983; Johnson and Ferrieri, 1984; Lindahl *et al.*, 1990; Russell-Jones *et al.*, 1984) and to complement regulator Factor H (FH), which avoid C3b deposition on GBS surface (Areschoug *et al.*, 2002). The binding site for IgA has been located to the N-terminal half of the protein, while the FH-binding region is at the C-terminal half of Bac (Areschoug *et al.*, 2002; Jarva *et al.*, 2002). Bac is structurally related to the pneumococcal Hic protein, and they bind FH in an analogous fashion (Janulczyk *et al.*, 2000; Jarva *et al.*, 2004).

[06] On the other hand, GAS acquires FH by M proteins and Fba, which contributes to the bacterium's capacity to evade phagocytosis by polymorphonuclear cells (Horstmann *et al.*, 1988; Pandiripally *et al.*, 2002; Pandiripally *et al.*, 2003). M-proteins also mediate acquisition of C4 binding protein (C4bp), an important regulator of complement classical pathway component C3 convertase (C4b2a) (Berggard *et al.*, 2001; Blom *et al.*, 2004). M protein binding to C4b has both decay accelerating activity and cofactor activity for C4b cleavage in an analogous fashion as FH in the alternative pathway (Carlsson *et al.*, 2005; Perez-Caballero *et al.*, 2004; Thern *et al.*, 1995).

[07] GAS and GBS also secrete the C5a peptidase, a multifunctional enzyme that inactivates human C5a (Jarva *et al.*, 2003; Wexler *et al.*, 1985) and binds fibronectin, which promotes bacterial invasion of epithelial cells (Beckmann *et al.*, 2002; Cheng *et al.*, 2002).

[08] Serum resistance factors are thought to play a role in mechanisms these gram positive bacteria use to evade the host immune response. There is, therefore, a continuing need in the art for identification of novel serum resistance factors in gram positive bacteria which can be used to develop compositions for the prevention or treatment of bacterial infection.

BRIEF DESCRIPTION OF THE FIGURES

[09] **FIG. 1A.** Diagram of BibA inserted in the cell membrane. **FIG. 1B**, Comparison of BibA and M protein structures.

[10] **FIG. 2A**. Domains of BibA proteins in different GBS strains. **FIG. 2B.** Representation of BibA cloned fragments, based on predicted functional domains.

[11] **FIGS. 3A-B.** Results of experiments demonstrating that recombinant BibA protein forms dimers. **FIG. 3A**, Gel-filtration of recombinant BibA; **FIG. 3B**, Coomassie staining.

[12] **FIGS. 4A-B**. BibA protein surface-association in GBS strains. **FIG. 4A**, strains 2603, 18RS21, and H36B. **FIG. 4B**, strains 515 and CJB111.

[13] **FIGS. 5A-B**. Data demonstrating that BibA protein is associated with the bacterial cell membrane or in the supernatant of GBS cultures. **FIG. 5A**, FACS analysis and Western blot (strains 2603 type V and 18RS21 type II; **FIG. 5B**, FACS analysis and Western blot (strain H36B type 1b).

[14] **FIG. 6**. Micrographs showing immunogold staining of strain 515, which expresses BibA protein of the 2603 V/R strain.

[15] **FIG. 7A**. Drawing showing BibA gene from strain 2063 cloned into pAM401 vector. **FIG. 7B**. FACS analysis demonstrating that BibA is expressed on the surface of strain 515 pAM401.

[16] **FIG. 8A**. FACS analysis demonstrating increased BibA expression on the surface of strain 2603. **FIG. 8B**, FACS analysis demonstrating BibA expression on the surface of strain 515.

[17] **FIG. 9**. FACS analysis demonstrating human-IgA-FITC binding to the surface of 2603-BibA overexpressing mutant strain.

[18] **FIGS. 10A-E**. Data demonstrating portions of BibA associated with the bacterial cell membrane or in the supernatant of GBS cultures. **FIG. 10A**, strain 515 type 1a; **FIG. 10B**, strain CJB111 type V; **FIG. 10C**, strain 2603 V/R; **FIG. 10D**, strain 18RS21; **FIG. 10E**, strain H36B.

[19] **FIGS. 11A-B**. Blots showing that BibA binds to C4 binding protein (C4BP). **FIG. 11A**, dot blot of native GBS proteins and GBS M1 protein overlaid with C4BP and probed with anti-C4BP antibody; **FIG. 11B**, Western blot analysis of recombinant GBS proteins overlaid with C4BP and probed with anti-C4BP antibody (left, Ponceau staining).

[20] **FIG. 12**. FACS analysis of BibA binding to the surface of various epithelial cells.

[21] **FIG. 13**. FACS analysis of BibA fragment binding to epithelial cells.

[22] **FIGS. 14A-C**. Western blots of BibA protein overlaid with purified human IgG and probed with anti-human IgG-HRP conjugated antibody. **FIG. 14A**, 7.5pMol of each protein overlaid with 5 mg/ml purified human IgG; **FIG. 14B**, 7.5pMol of each protein overlaid with 1 mg/ml purified human IgG; **FIG 14C**, 15 pMol = BibA overlaid with 5 μg/ml purified human IgG.

[23] **FIG. 15**. Blots showing that purified human-IgA binds to BibA protein. Left two blots, Western blot analysis of denatured BibA overlaid with purified human IgA-HRP. Right blot, dot blot analysis of native BibA overlaid with purified human IgA-HRP.

[24] **FIG. 16**. Western blot showing binding of tryptic digested fragments of BibA to IgA.

[25] **FIGS. 17A-C**. Blots demonstrating that BibA-His is specific for human and rabbit IgG. **FIG. 17A**, human serum goat-α-human-IgG-HRP; **FIG. 17B**, rabbit serum goat-α-rabbit-IgG-HRP; **FIG. 17C**, mouse serum rabbit-α-mouse-IgG-HRP.

[26] **FIG. 18**. Western blot showing that BibA binds to human IgG (lane C), human serum IgA (lane E) and C4BP (lane G). M protein of GBS was used as positive control (lanes D, F, H).

[27] **FIGS. 19A-L.** Data demonstrating that BibA is expressed as surface exposed and secreted in GBS strain 2603 V/R. **FIG. 19A**, flow cytometry analysis of BibA on the surface of 2603 V/R GBS strain. Bacteria were incubated with a polyclonal mouse anti-BibA antibody and stained with FITC-conjugated anti-mouse IgG antibody black line histogram. The dashed line histogram indicates bacteria treated with primary and secondary antibodies alone.

[28] **FIG. 19B**, immunogold electron microscopy of BibA expression on GBS strains 2603 V/R. Bacteria were absorbed to formvar-carbon-coated nickel grids and then fixed in 2% PFA. The grids were floated on drops of primary antiserum anti-BibA protein and then on secondary antibody conjugated to 10-nm gold particles.

[29] **FIG. 19C**, Western blot analysis of the presence of BibA in protein extracts from GBS strain 2603 V/R. P Peptidoglycan associated protein fraction and S Bacterial supernatant protein fraction. GBS protein fractions were separated on SDS-10% PAGE gels and transferred to nitrocellulose membrane. Proteins were overlaid with a mouse anti-BibA polyclonal antibody and stained with HRP-conjugated antibody. Positive bands were detected by ECL.

[30] **FIG. 19D**, flow cytometry analysis of BibA on the surface of strain 2603Δ*bibA*. Bacteria were incubated with a polyclonal mouse anti-BibA antibody and stained with FITC-conjugated anti-mouse IgG antibody black line histogram. The dashed line histogram indicates bacteria treated with primary and secondary antibodies alone.

[31] **FIG. 19E**, immunogold electron microscopy of BibA expression on GBS strains 2603Δ*bibA*. Bacteria were absorbed to formvar-carbon-coated nickel grids and then fixed in 2% PFA. The grids were floated on drops of primary antiserum anti-BibA protein and then on secondary antibody conjugated to 10-nm gold particles.

[32] **FIG. 19F**, flow cytometry analysis of BibA on the surface of strain 515 Ia. Bacteria were incubated with a polyclonal mouse anti-BibA antibody and stained with FITC-conjugated

anti-mouse IgG antibody black line histogram. The dashed line histogram indicates bacteria treated with primary and secondary antibodies alone.

[33] **FIG. 19G**, immunogold electron microscopy of BibA expression on GBS strains 515 Ia. Bacteria were absorbed to formvar-carbon-coated nickel grids and then fixed in 2% PFA. The grids were floated on drops of primary antiserum anti-BibA protein and then on secondary antibody conjugated to 10-nm gold particles.

[34] **FIG. 19H**, Western blot analysis of the presence of BibA in protein extracts from GBS strains 515 Ia and 515pAM401*bibA*. P Peptidoglycan associated protein fraction and S Bacterial supernatant protein fraction. GBS protein fractions were separated on SDS-10% PAGE gels and transferred to nitrocellulose membrane. Proteins were overlaid with a mouse anti-BibA polyclonal antibody and stained with HRP-conjugated antibody. Positive bands were detected by ECL.

[35] **FIG. 19I**, flow cytometry analysis of BibA on the surface of strain 515pAM401bibA. Bacteria were incubated with a polyclonal mouse anti-BibA antibody and stained with FITC-conjugated anti-mouse IgG antibody black line histogram. The dashed line histogram indicates bacteria treated with primary and secondary antibodies alone.

[36] **FIG. 19L**, immunogold electron microscopy of BibA expression on GBS strains 515pAM401*bibA*. Bacteria were absorbed to formvar-carbon-coated nickel grids and then fixed in 2% PFA. The grids were floated on drops of primary antiserum anti-BibA protein and then on secondary antibody conjugated to 10-nm gold particles.

[37] **FIGS. 20A-F**. Western blots demonstrating that BibA binds to human immunoglobulins. **FIG. 20A**, recombinant BibA separated on SDS PAGE and blotted on nitrocellulose membrane. The membrane was then overlaid with 0.5 μg/ml human, mouse or bovine purified serum IgG and positive binding to IgG revealed by secondary antibodies versus the different IgG species. To evaluate the binding ECL detection was performed. M1 protein of GBS was used as positive control, while GBS104 was used as a non-specific

binding control. **FIG. 20B** as in **FIG. 20A** apart from testing the binding to human serum or secretory IgA, overlaid at a concentration of 0.5 μg/ml. The blots are representative of experiments performed at least in triplicate. **FIG. 20C** and **FIG. 20D** Different concentrations of purified recombinant BibA in PBS were spotted on a nitrocellulose membrane and overlay assay performed as in **FIG. 20A**. **FIG. 20C**, overlay with human serum IgG. **FIG. 20D**, overlay with human serum IgA. **FIG. 20E**, overlay blotting with human IgG of SDS-PAGE separated N-terminal and C-terminal constructs of BibA. **FIG. 20F**, overlay blotting with human IgA of SDS-PAGE separated N-terminal and C-terminal constructs of BibA.

[38] **FIGS. 21A-C.** Data demonstrating that BibA binds to human C4BP. **FIG. 21A**, recombinant BibA separated on SDS PAGE and blotted on nitrocellulose membrane. The membrane was overlaid with 5 μg/ml human C4BP and binding revealed by secondary antibodies versus C4BP. M1 protein of GBS was used as positive control, while GBS201 as non-specific binding control. **FIG. 21B**, dot blot of different concentrations of native recombinant BibA spotted on nitrocellulose membrane and overlaid with 5 μg/ml C4BP as in FIG. 21A. **FIG. 21C**, Western blot of SDS-PAGE separated N-terminal and C-terminal constructs of BibA overlaid with human C4BP. Experimental blotting conditions as in **FIG. 21A**.

[39] **FIGS. 22A-C.** Graphs demonstrating binding of recombinant BibA to epithelial cells. **FIG. 22A**, ME180 cells were incubated for 1h at 4°C with increasing concentrations of recombinant BibA range 0.01-62.5 μg/ml. Then cells were washed and incubated with mouse anti-BibA antibodies followed by FITC-conjugated secondary anti-mouse antibodies. MFI Mean fluorescence intensity. The plot is representative of three independent experiments. **FIG. 22B**, saturation curve of BibA binding to ME180 cells. Analysis was performed on data reported on panel A. The Kd value was calculated as the BibA concentration that determines the saturation of 50% of the receptors present on cells. **FIG. 22C**, representative flow cytometric profiles of the binding of 10 μg/ml BibA

to A549, Caco2 and 16HBE epithelial cells. Binding experimental conditions and analysis as in **FIG. 22A**. Dashed-line histograms represent the MFI of control cells.

[40] **FIGS. 23A-F**. Data demonstrating that BibA expression modulates GBS capacity to adhere to epithelial cells. **FIG. 23A**, ME180 cells grown in a 24 well plate were infected with GBS strains 2603 V/R, 2603Δ*bibA* and 2603pAM401*bibA* for 3 hours. Non-adherent bacteria were gently washed off and cells lysed with saponin for association assay. The white column indicates the percentage of associated bacteria in the wild type strain, the light grey column indicates the percentage of association of the BibA isogenic mutant strain and the dark grey column the association of the wild type strain overexpressing BibA. **FIG. 23B**, as in **FIG. 23A** except that infection was carried out in A549 cells. Mean values ± standard deviations of three individual experiments. Data evaluated by Student's T-test, were 95% confident.

[41] **FIG. 23C**, micrographs of confocal imaging analysis of the 2603 V/R strain association to A549 lung epithelial cells in comparison to the isogenic mutant strain lacking BibA gene (**FIG. 23D**). A549 cells were grown on glass slides were infected with GBS for 3h. Bacteria were then stained with mouse polyclonal antisera raised against type V capsular polysaccharide and rabbit polyclonal anti-BibA antibodies. Capsule and BibA were respectively labeled with Alexa Fluor 562 red and 488 green conjugated secondary antibody. A549 cells F-actin was labeled with Alexa Fluor 622 conjugated phalloidin blue. The results shown in the figure are typical of multiple experiments.

[42] **FIG. 23E**, confocal imaging analysis of the 515 Ia wild type strain and the isogenic strain carrying a plasmid containing the 515 pAM401*bibA* gene (**FIG. 23F**) in association to A549 epithelial cells.

[43] **FIG. 24**. Overview of sequence organization of BibA proteins. N-terminal domains are predicted to form helix-rich structures, according to prediction obtained using the Paircoil program Berger *et al.*, 1995 at Expasy web server (domain name expasy.org). Positions

of classical LPXTG (SEQ ID NO:3) cell wall anchoring motif and trans-membrane domain are also indicated.

[44] **FIG. 25**. Summary of data demonstrating that BibA is involved in GBS adherence to epithelial cells.

[45] **FIG. 26**. Summary of data demonstrating that BibA overexpression increases GBS adherence to epithelial cells.

[46] **FIG. 27**. Summary of data demonstrating that expression of BibA on 515 Ia surface increases adherence to epithelial cells.

[47] **FIG. 28**. Summary of data demonstrating that IgA binds to the N-terminal portion of recombinant BibA.

[48] **FIG. 29**. Summary of data demonstrating that the IgA binding domain is contained within the first 200 amino acids of BibA.

[49] **FIG. 30**. BibA promotes GBS survival of PMN killing. Human neutrophils were incubated for 3 hours with GBS 2603 V/R and 2603Δ*bibA* mutant strains (MOI 1:1) in the presence of human serum (white bars) or complement inactivated human serum (grey bars). Percentage of viable bacteria after incubation with neutrophils is reported. A typical experiment performed in triplicate is shown. The experiment was repeated at least three times with similar results.

DETAILED DESCRIPTION OF THE INVENTION

[50] Applicants have identified a serum resistance factor in a gram positive bacteria (GBS) which interacts with host cell complement pathways and is thought to be involved in the invading bacteria's complement resistance or evasion mechanisms. This newly identified serum resistance factor is referred to herein as group B streptococcus immunoglobulin-

binding adhesion (BibA) (also known as GBS 3). BibA is a widely expressed protein, present in 81% of the 31 strains of GBS analyzed (**Table 3**).

[51] A BLAST search against the non-redundant GenBank database revealed a low similarity of the BibA N-terminal region with a series of gram positive immunoglobulin-binding proteins such as the M-protein family of *S. pyogenes* (22% identity), Bac of *S. agalactiae* (20% identity), PspC of *S. pneumoniae* (20% identity), and Mig of *S. dysagalactiae* (27% identity). BibA shares some similarities with resistance factors of other gram-positive bacteria, such as the Hic-like proteins of *S. pneumoniae*.

[52] The *bibA* gene is located between s*ecE* and *nusG* genes. *SecE* and *nusG* are co-transcribed in *E. coli* (Downing *et al.*, 1990) and are adjacent in a large panel of gram positive and gram negative bacteria (Barreiro *et al.*, 2001; Fuller *et al.*, 1999; Jeong *et al.*, 1993; Katayama *et al.*, 1996; Miyake *et al.*, 1994; Poplawski *et al.*, 2000; Puttikhunt *et al.*, 1995; Sharp, 1994; Syvanen *et al.*, 1996). This evidence suggests that the present genomic localization of BibA is likely to derive from an insertion event. Of interest, two transposases present in A909 strain are members of the IS1381 family, which has been proposed as a tool for GBS subtyping (Tamura *et al.*, 2000) and whose presence has been correlated with the evolution of the *S. agalactiae* species analyzed by multilocus sequence typing (MLST) (Hery-Arnaud *et al.*, 2005).

[53] *In silico* analysis of the seven GBS completed genomes revealed that BibA is a modular protein; its sequence variability is mainly due to a different number of short amino acid repeats either in N-terminal or the C-terminal domains. Full-length BibA comprises an N-terminal helix-rich region, a C-terminal proline-rich region, a LPXTG (SEQ ID NO:3) motif that anchors the protein to the cell wall peptidoglycan, and a transmembrane domain. **FIGS. 1A, 2B**. The coiled-coil domain of BibA is well conserved across multiple serotypes of *S. agalactiae*.

[54] BibA is structurally related to the family of M-like proteins of *S. pyogenes* (GBS) (**FIG. 1B**). The secondary structure of M proteins is primarily an α-helical coiled coil structure

which forms stable dimers (Phillips *et al.*, 1981). *In silico* prediction of BibA secondary structure (Berger *et al.*, 1995) reveals in the N-terminal region a helix-rich region with the propensity to form a coiled-coil arrangement (regions 283-294 and 366-400). Studies on the recombinant form of BibA suggest that, as for M proteins, BibA is able to form dimers, which are opened in non-reducing conditions. No canonical elements of secondary structure are on the contrary predicted within the proline-rich region, which suggests that this part of the molecule could adopt a poly-proline helix-like conformation.

[55] BibA is expressed on the surface of several GBS strains, but is also recovered in GBS culture supernatants. BibA, whether expressed on the cell wall or secreted in the supernatant fractions, has an identical apparent molecular weight. This suggests that secretion of BibA might be due to either a proteolytic cleavage of the cell-wall anchoring domain or that an impaired sorting of the protein could be responsible for the secretion. Indeed, BibA has an YSSIRK-G/S-like motif (SEQ ID NO:64) in the signal peptide, which has previously been described to be present in *Staphylococcus aureus* and other gram positive pathogens (Bae and Schneewind, 2003). Such a motif is exclusively present in BibA and is conserved in all the eight GBS strains analyzed. The YSSIRK-G/S-like motif (SEQ ID NO:64) has been postulated to be involved in accelerating protein maturation (Bae and Schneewind, 2003). Based on this evidence, we hypothesize that sortase components may be limiting for complete and efficient anchoring of BibA, which results in the incomplete processing of mature BibA and the release of the protein in the supernatant.

[56] Functional characterization identifies BibA as a member of a group of streptococcal surface-exposed multifunctional proteins which mediate bacterial colonization and modulate host immune-response (Jarva *et al.*, 2003; Lindahl *et al.*, 2005). However, BibA has unique features, such as the binding both to human immunoglobulins and to complement regulator C4bp. The BibA binding site for IgA and C4bp resides in the N-terminal region of the protein. However, there is no homology to the Bac N-terminal domain specific for IgA (Lindahl *et al.*, 1990). The lack of binding to mouse and bovine

IgG suggests that BibA has a human specific functional role, as reported for other Ig-binding proteins.

[57] Secreted BibA binds to human epithelial cells, complement (such as C4 binding protein), and specifically to human IgG and IgA. The proline-rich domain of secreted BibA is responsible for the binding interaction with human epithelial cells. **Examples 8, 9**. The proline-rich domain has a periodicity of 8 amino acids. Proline occupies positions b and f of the motif, which is repeated 19 times:

399-(aK**P**DVK**P**EAh)	(SEQ ID NO:9)
(K**P**EAK**P**DV)6	(SEQ ID NO:10)
K**P**KAK**P**DV	(SEQ ID NO:11)
K**P**EAK**P**DV	(SEQ ID NO:10)
K**P**DVK**P**DV	(SEQ ID NO:12)
K**P**EAK**P**ED	(SEQ ID NO:13)
K**P**DVK**P**DV	(SEQ ID NO:12)
K**P**EAK**P**DV	(SEQ ID NO:10)
(K**P**EAK**P**EA)3	(SEQ ID NO:14)
(K**P**DVK**P**EA)2	(SEQ ID NO:15)
K**P**EAK**P**EA-551	(SEQ ID NO:14)

[58] The proline-rich domain, when present, is located towards the C-terminus of BibA. As illustrated in **FIG. 2A**, the proline-rich domain is generally located from amino acid 400 to the end of the C-terminus.

[59] To elucidate the BibA binding region to immunoglobulins, we generated two constructs comprising the N-terminal or the C-terminal portion of the protein. BibA binding to human IgG resides predominantly in the N-terminal region of the protein, while the C-terminal region binds to a lower extent. On the other hand, the binding to human IgA was exclusively associated to the N-terminal portion of BibA. This region was also responsible for the binding of BibA to the C4bp. In addition, recombinant BibA binds to human epithelial cells of different origin, with an affinity constant of $\sim 10^{-8}$ M.

[60] The coiled-coil domain is well-conserved in various GBS strains. The coiled-coil domain is responsible for the binding interaction of BibA with complement such as C4 binding protein. **Example 7.** The coiled-coil domain is also responsible for binding interactions with human immunoglobulins, such as IgG and IgA. **Examples 10, 11,** and **12.** The IgA binding site appears to be in the N-terminal portion (roughly 200 amino acids) of BibA. BibA, like other coiled-coil proteins, forms dimers. **Example 1.**

[61] When bacteria secrete BibA, it is believed that the proline-rich C terminus domain of the protein binds to host epithelial cells, leaving the N-terminal coiled-coil domain exposed to serum factors. The N-terminal coiled-coil domain is then thought to attract complement, such as C4 binding protein, diverting it away from the invading bacteria. Complement binding interaction with the host cell attached coiled-coil domain attracts complement activity to the host cell, further facilitating bacterial invasion.

[62] In some strains the LPXTG (SEQ ID NO:3)/proline-rich domain is absent. **FIG. 2A.** When the proline-rich domain is absent or expressed separately, BibA is thought to be primarily secreted, and not surface exposed. However, even truncated or bifurcated forms of BibA are thought to divert immune system attention away from the bacterium as it approaches target host cells.

[63] The role of BibA in GBS adhesion to cells was confirmed by the impaired ability of a BibA knock-out mutant strain to bind to both human cervical and lung epithelial cells. Complementation of the mutation restored GBS adhesive phenotype, while BibA over-expression significantly increased the binding to epithelial cells. These characteristics indicate that BibA is a novel multifunctional protein and is likely involved in GBS pathogenicity.

[64] The soluble form of BibA protein has an apparent molecular weight on an SDS polyacrylamide gel of ~80kDa, although its expected molecular weight is ~60kDa. The proline-rich domain of the protein is likely to be responsible for this shift, due to the folding of BibA into a bundled-like shape. The membrane-associated form is easily

degraded; a small fraction of the protein runs on a gel as an 80kD, while the major fraction runs at a MW of ~60kDa. This indicates that in the membrane-associated form the proline-rich motif is still associated with the cell wall components and maintains a linear structure. See **Examples 2-4, 6.**

[65] Bacterial adherence to host cells is the initial step and a prerequisite for successful colonization of host mucosal surfaces. The analysis of the binding of recombinant BibA to epithelial cells revealed that the association to cells could be saturated, with an estimated affinity constant of $\approx 4x10^{-8}$ M. In particular, BibA binding to epithelial cell lines of lung, intestine, bronchus and cervix origin, suggests the existence of an ubiquitous receptor. BibA, like M-proteins (Courtney *et al.*, 1994; Courtney *et al.*, 1997; Wang and Stinson, 1994), mediates bacterial adhesion to epithelial cells. Studies of isogenic BibA-positive and BibA-negative strains indicated that the BibA-positive strain adhered to epithelial cells, while the BibA-negative strain showed greatly reduced adherence. In addition, expression of the cell-wall anchored form of BibA in a strain not exposing BibA on the surface increased its associative phenotype. Of interest, such results were confirmed in both human cervical (ME180) and lung (A549) epithelial cell lines, which are a target for GBS colonization.

[66] These functional properties suggest that BibA is a serum resistance factor involved in GBS pathogenicity and is therefore useful as an active agent in compositions for preventing and for treating *S. agalactiae* infections.

I. BibA polypeptides

[67] "BibA polypeptides" of the invention comprise a portion of a BibA protein which consists of (1) a coiled-coil domain of the BibA protein; (2) a leader sequence and the coiled-coil domain of the BibA protein; (3) a proline-rich domain of the BibA protein; (4) the coiled-coil and proline-rich domains of the BibA protein; or (5) the leader sequence, the coiled-coil domain, and the proline-rich domain of the BibA protein and are free of

other contiguous amino acid sequences of the BibA protein. BibA polypeptides of the invention do not comprise the amino acid sequence of a full-length BibA polypeptide.

[68] BibA polypeptides include those polypeptides identified as "I," "II," and "III" in **FIG. 24.**

[69] BibA protein from GBS serotype V isolated strain 2603 V/R has the amino acid sequence shown in SEQ ID NO:1:

MNNNEKKVKYFLRKTAYGLASMSAAFAVCSGIVHADTSSGISASIPHKKQVNLGAVTLKNLISKYRGNDKAIAILL
SRVNDFNRASQDTLPQLINSTEAEIRNILYQGQIGKQNKPSVTTHAKVSDQELGKQSRRSQDIIKSLGFLSSDQKD
ILVKSISSSKDSQLILKFVTQATQLNNAESTKAKQMAQNDVALIKNISPEVLEEYKEKIQRASTKSQVDEFVAEAK
KVVNSNKETLVNQANGKKQEIAKLENLSNDEMLRYNTAIDNVVKQYNEGKLNITAAMNALNSIKQAAQEVAQKNLQ
KQYAKKIERISSKGLALSKKAKEIYEKHKSILPTPGYYADSVGTYLNRFRDKQTFGNRSVWTGQSGLDEAKKMLDE
VKKLLKELQDLTRGTKEDKKPDVKPEAKPEAKPDVKPEAKPDVKPEAKPDVKPEAKPDVKPEAKPDVKPEAKPDVK
PKAKPDVKPEAKPDVKPDVKPDVKPEAKPEDKPDVKPDVKPEAKPDVKPEAKPEAKPEAKPEAKPEAKPDVK
PEAKPDVKPEAKPEAKPEAKSEAKPEAKLEAKPEAKPATKKSVNTSGNLAAKKAIENKKYSKK***LPSTG***EAASPLLA
IVSLIVMLSAGLITIVLKHKKN

[70] BibA contains an N-terminal leader or signal sequence domain which is indicated by the underlined sequence at the beginning of SEQ ID NO:1 above and the C-terminal transmembrane domain which is indicated by the underlined sequence at the end of SEQ ID NO:1 above. One or more amino acids from the leader or signal sequence domain of BibA may be removed. An example of such a BibA fragment is set forth below as SEQ ID NO:2:

TSSGISASIPHKKQVNLGAVTLKNLISKYRGNDKAIAILLSRVNDFNRASQDTLPQLINSTEAEIRNILYQGQI
GKQNKPSVTTHAKVSDQELGKQSRRSQDIIKSLGFLSSDQKDILVKSISSSKDSQLILKFVTQATQLNNAESTK
AKQMAQNDVALIKNISPEVLEEYKEKIQRASTKSQVDEFVAEAKKVVNSNKETLVNQANGKKQEIAKLENLSND
EMLRYNTAIDNVVKQYNEGKLNITAAMNALNSIKQAAQEVAQKNLQKQYAKKIERISSKGLALSKKAKEIYEKH
KSILPTPGYYADSVGTYLNRFRDKQTFGNRSVWTGQSGLDEAKKMLDEVKKLLKELQDLTRGTKEDKKPDVKPE
AKPEAKPDVKPEAKPDVKPEAKPDVKPEAKPDVKPEAKPDVKPEAKPDVKPKAKPDVKPEAKPDVKPDVKPDVK
PEAKPEDKPDVKPDVKPEAKPDVKPEAKPEAKPEAKPEAKPEAKPDVKPEAKPDVKPEAKPEAKPEAKSE
AKPEAKLEAKPEAKPATKKSVNTSGNLAAKKAIENKKYSKKLPSTGEAASPLLAIVSLIVMLSAGLITIVLKHK
KN

[71] BibA also contains an amino acid motif indicative of a cell wall anchor:

LPXTG (SEQ ID NO:3, shown in bold and italics in SEQ ID NO:1 above).

[72] In one embodiment, the leader or signal sequence domain, the transmembrane and cytoplasmic domains, and the cell wall anchor motif are removed from the BibA sequence to leave the coiled-coil and proline-rich segments as set forth below as SEQ ID NO:4:

TSSGISASIPHKKQVNLGAVTLKNLISKYRGNDKAIAILLSRVNDFNRASQDTLPQLINSTEAEIRNILYQGQI
GKQNKPSVTTHAKVSDQELGKQSRRSQDIIKSLGFLSSDQKDILVKSISSSKDSQLILKFVTQATQLNNAESTK
AKQMAQNDVALIKNISPEVLEEYKEKIQRASTKSQVDEFVAEAKKVVNSNKETLVNQANGKKQEIAKLENLSND
EMLRYNTAIDNVVKQYNEGKLNITAAMNALNSIKQAAQEVAQKNLQKQYAKKIERISSKGLALSKKAKEIYEKH
KSILPTPGYYADSVGTYLNRFRDKQTFGNRSVWTGQSGLDEAKKMLDEVKKLLKELQDLTRGTKEDKKPDVKPE
AKPEAKPDVKPEAKPDVKPEAKPDVKPEAKPDVKPEAKPDVKPKAKPDVKPEAKPDVKPDVKPDVK
PEAKPEDKPDVKPDVKPEAKPDVKPEAKPEAKPEAKPEAKPDVKPEAKPDVKPEAKPEAKPEAKSE
AKPEAKLEAKPEAKPATKKSVNTSGNLAAKKAIENKKYSKK

[73] The proline-rich domain of BibA is indicated below as SEQ ID NO:5.

PDVKPEAKPDVKPEAKPDVKPKAKPDVKPEAKPDVKPDVKPDVKPEAKPEDKPDVKPDVKPEAKPDVKPEAKPEAKP
EAKPEAKPEAKPEAKPDVKPEAKPDVKPEAKPEAKPEAKSEAKPEAKLEAKPEAKPATKKSVNTSGNLAAKKAIENK
KYSKK

[74] The coiled-coil domain and signal peptide domain of BibA are set forth below as SEQ ID NO:6:

MNNNEKKVKYFLRKTAYGLASMSAAFAVCSGIVHADTSSGISASIPHKKQVNLGAVTLKNLISKYRGNDKAIAILL
SRVNDFNRASQDTLPQLINSTEAEIRNILYQGQIGKQNKPSVTTHAKVSDQELGKQSRRSQDIIKSLGFLSSDQKD
ILVKSISSSKDSQLILKFVTQATQLNNAESTKAKQMAQNDVALIKNISPEVLEEYKEKIQRASTKSQVDEFVAEAK
KVVNSNKETLVNQANGKKQEIAKLENLSNDEMLRYNTAIDNVVKQYNEGKLNITAAMNALNSIKQAAQEVAQKNLQ
KQYAKKIERISSKGLALSKKAKEIYEKHKSILPTPGYYADSVGTYLNRFRDKQTFGNRSVWTGQSGLDEAKKMLDE
VKKLLKELQDLTRGTKEDKKPDVKPEAKPEAKPDVKPEAKPDVKPEAKPDVKPEAK

[75] The highly conserved coiled-coil domain of BibA is located towards the N-terminus of the protein and is underlined in the BibA SEQ ID NO:1 sequence below. The underlined

fragment corresponding to the coiled-coil domain of BibA is set forth below as SEQ ID NO:7:

SEQ ID NO:1

MNNNEKKVKYFLRKTAYGLASMSAAFAVCSGIVHADTSSGISASIPHKKQVNLGAVTLKNLISKYRGNDKAIAILL
SRVNDFNRASQDTLPQLINSTEAEIRNILYQGQIGKQNKPSVTTHAKVSDQELGKQSRRSQDIIKSLGFLSSDQKD
ILVKSISSSKDSQLILKFVTQATQLNNAESTKAKQMAQNDVALIKNISPEVLEEYKEKIQRASTKSQVDEFVAEAK
KVVNSNKETLVNQANGKKQEIAKLENLSNDEMLRYNTAIDNVVKQYNEGKLNITAAMNALNSIKQAAQEVAQKNLQ
KQYAKKIERISSKGLALSKKAKEIYEKHKSILPTPGYYADSVGTYLNRFRDKQTFGNRSVWTGQSGLDEAKKMLDE
VKKLLKELQDLTRGTKEDKKPDVKPEAKPEAKPDVKPEAKPDVKPEAKPDVKPEAKPDVKPEAKPDVKPEAKPDVK
PKAKPDVKPEAKPDVKPDVKPDVKPEAKPEDKPDVKPDVKPEAKPDVKPEAKPEAKPEAKPEAKPEAKPDVK
PEAKPDVKPEAKPEAKPEAKSEAKPEAKLEAKPEAKPATKKSVNTSGNLAAKKAIENKKYSKKLPSTGEAASPLLA
IVSLIVMLSAGLITIVLKHKKN

SEQ ID NO:7

TSSGISASIPHKKQVNLGAVTLKNLISKYRGNDKAIAILLSRVNDFNRASQDTLPQLINSTEAEIRNILYQGQI
GKQNKPSVTTHAKVSDQELGKQSRRSQDIIKSLGFLSSDQKDILVKSISSSKDSQLILKFVTQATQLNNAESTK
AKQMAQNDVALIKNISPEVLEEYKEKIQRASTKSQVDEFVAEAKKVVNSNKETLVNQANGKKQEIAKLENLSND
EMLRYNTAIDNVVKQYNEGKLNITAAMNALNSIKQAAQEVAQKNLQKQYAKKIERISSKGLALSKKAKEIYEKH
KSILPTPGYYADSVGTYLNRFRDKQTFGNRSVWTGQSGLDEAKKMLDEVKKLLKELQDLTRGTKEDKK

[76] The signal peptide (amino acids 1-36), coiled coil domain, and proline-rich domain of BibA are set forth below in SEQ ID NO:8:

MNNNEKKVKYFLRKTAYGLASMSAAFAVCSGIVHADTSSGISASIPHKKQVNLGAVTLKNLISKYRGNDKAIAILL
SRVNDFNRASQDTLPQLINSTEAEIRNILYQGQIGKQNKPSVTTHAKVSDQELGKQSRRSQDIIKSLGFLSSDQKD
ILVKSISSSKDSQLILKFVTQATQLNNAESTKAKQMAQNDVALIKNISPEVLEEYKEKIQRASTKSQVDEFVAEAK
KVVNSNKETLVNQANGKKQEIAKLENLSNDEMLRYNTAIDNVVKQYNEGKLNITAAMNALNSIKQAAQEVAQKNLQ
KQYAKKIERISSKGLALSKKAKEIYEKHKSILPTPGYYADSVGTYLNRFRDKQTFGNRSVWTGQSGLDEAKKMLDE
VKKLLKELQDLTRGTKEDKKPDVKPEAKPEAKPDVKPEAKPDVKPEAKPDVKPEAKPDVKPEAKPDVKPEAKPDVK
PKAKPDVKPEAKPDVKPDVKPDVKPEAKPEDKPDVKPDVKPEAKPDVKPEAKPEAKPEAKPEAKPEAKPDVKP
EAKPDVKPEAKPEAKPEAKSEAKPEAKLEAKPEAKPATKKSVNTSGNLAAKKAIENKKYSKK

II. Nucleic acid molecules encoding BibA polypeptides

[77] The invention includes nucleic acid molecules which encode BibA polypeptides. The invention also includes nucleic acid molecules comprising nucleotide sequences having at least 50% sequence identity to such molecules. Depending on the particular sequence, the degree of sequence identity is preferably greater than 50% (e.g., 60%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or more). Identity between nucleotide sequences is preferably determined by the Smith-Waterman

homology search algorithm as implemented in the MPSRCH program (Oxford Molecular), using an affine gap search with parameters gap open penalty = 12 and gap extension penalty = 1.

[78] The invention also provides nucleic acid molecules which can hybridize to these molecules. Hybridization reactions can be performed under conditions of different "stringency." Conditions which increase stringency of a hybridization reaction are widely known and published in the art. *See, e.g.*, page 7.52 of Sambrook et al., Molecular Cloning: A Laboratory Manual, 1989. Examples of relevant conditions include (in order of increasing stringency): incubation temperatures of 25 °C, 37 °C, 50 °C, 55 °C, and 68 °C; buffer concentrations of 10X SSC, 6X SSC, 1X SSC, and 0.1X SSC (where SSC is 0.15 M NaCl and 15 mM citrate buffer) and their equivalents using other buffer systems; formamide concentrations of 0%, 25%, 50%, and 75%; incubation times from 5 minutes to 24 hours; 1, 2, or more washing steps; wash incubation times of 1, 2, or 15 minutes; and wash solutions of 6X SSC, 1X SSC, 0.1X SSC, or de-ionized water. Hybridization techniques and their optimization are well known in the art. *See, e.g.*, Sambrook, 1989; Ausubel *et al.*, eds., Short Protocols in Molecular Biology, 4th ed., 1999; U.S. Patent 5,707,829; Ausubel *et al.*, eds., Current Protocols in Molecular Biology, Supplement 30, 1987.

[79] In some embodiments, nucleic acid molecules of the invention hybridize to a target under low stringency conditions; in other embodiments, nucleic acid molecules of the invention hybridize under intermediate stringency conditions; in preferred embodiments, nucleic acid molecules of the invention hybridize under high stringency conditions. An example of a low stringency hybridization condition is 50 °C and 10X SSC. An example of an intermediate stringency hybridization condition is 55 °C and 1X SSC. An example of a high stringency hybridization condition is 68 °C and 0.1X SSC.

[80] Nucleic acid molecules comprising fragments of these sequences are also included in the invention. These comprise at least n consecutive nucleotides of these sequences and,

depending on the particular sequence, n is 10 or more (*e.g.*, 12, 14, 15, 18, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, 100, 150, 200, or more).

[81] Nucleic acids (and polypeptides) of the invention may include sequences which:

(a) are identical (i.e., 100% identical) to the sequences disclosed in the sequence listing;

(b) share sequence identity with the sequences disclosed in the sequence listing;

(c) have 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 single nucleotide or amino acid alterations (deletions, insertions, substitutions), which may be at separate locations or may be contiguous, as compared to the sequences of (a) or (b); and,

(d) when aligned with a particular sequence from the sequence listing using a pairwise alignment algorithm, a moving window of x monomers (amino acids or nucleotides) moving from start (N-terminus or 5′) to end (C-terminus or 3′), such that for an alignment that extends to p monomers (where p>x) there are p-x+1 such windows, each window has at least x·y identical aligned monomers, where: x is selected from 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 150, 200; y is selected from 0.50, 0.60, 0.70, 0.75, 0.80, 0.85, 0.90, 0.91, 0.92, 0.93, 0.94, 0.95, 0.96, 0.97, 0.98, 0.99; and if x·y is not an integer then it is rounded up to the nearest integer. The preferred pairwise alignment algorithm is the Needleman-Wunsch global alignment algorithm [Needleman & Wunsch (1970) J. Mol. Biol. 48, 443-453], using default parameters (e.g., with Gap opening penalty = 10.0, and with Gap extension penalty = 0.5, using the EBLOSUM62 scoring matrix). This algorithm is conveniently implemented in the needle tool in the EMBOSS package [Rice et al. (2000) Trends Genet. 16:276-277].

[82] The nucleic acids and polypeptides of the invention may additionally have further sequences to the N-terminus/5′ and/or C-terminus/3′ of these sequences (a) to (d).

[83] Nucleic acid molecules of the invention can be single- or double-stranded and can be used, for example, to produce BibA polypeptides *in vitro* (*i.e.*, a recombinant protein) or *in vivo* (as a DNA vaccine). The invention also provides single-stranded nucleic acid molecules which can hybridize to other nucleic acid molecules of the invention, preferably under "high stringency" conditions (*e.g.*, 65°C in a 0.1xSSC, 0.5% SDS solution).

[84] Nucleic acid molecules of the invention can comprise DNA or RNA, including analogues, such as those containing modified backbones (*e.g.*, phosphorothioates, *etc.*), and also peptide nucleic acids (PNA), *etc.* Nucleic acid molecules of the invention can comprise portions of genomic DNA, cDNA, or mRNA. Nucleic acid molecules of the invention do not encode full-length BibA proteins.

[85] An example of a nucleic acid molecule which encodes a full-length BibA protein from which portions encoding BibA polypeptides can be derived is set forth below as SEQ ID NO:16:

ATGAATAATAACGAAAAAAAAGTAAAATACTTTTTAAGAAAAACAGCTTATGGTTTGGCCTCAATGTCAGCAGCGT
TTGCTGTATGTAGTGGTATTGTACACGCGGATACTAGTTCAGGAATATCGGCTTCAATTCCTCATAAGAAACAAGT
TAATTTAGGGGCGGTTACTCTGAAGAATTTGATTTCTAAATATCGTGGTAATGACAAAGCTATTGCTATACTTTTA
AGTAGAGTAAATGATTTTAATAGAGCATCACAGGATACACTTCCACAATTAATTAATAGTACTGAAGCAGAAATTA
GAAATATTTTATATCAAGGACAAATTGGTAAGCAAAATAAACCAAGTGTAACTACACATGCTAAAGTTAGTGATCA
AGAACTAGGTAAGCAGTCAAGACGTTCTCAAGATATCATTAAGTCATTAGGTTTCCTTTCATCAGACCAAAAAGAT
ATTTTAGTTAAATCTATTAGCTCTTCAAAAGATTCGCAACTTATTCTTAAATTTGTAACTCAAGCCACGCAACTGA
ATAATGCTGAATCAACAAAAGCTAAGCAAATGGCTCAAAATGACGTGGCCTTAATAAAAAATATAAGCCCCGAAGT
CTTAGAAGAATATAAAGAAAAAATTCAAAGAGCTAGCACTAAGAGTCAAGTTGATGAGTTTGTAGCAGAAGCTAAA
AAAGTTGTTAATTCCAATAAAGAAACGTTGGTAAATCAGGCCAATGGTAAAAAGCAAGAAATTGCTAAGTTAGAAA
ATTTATCTAACGATGAAATGTTGAGATATAATACTGCAATTGATAATGTAGTGAAACAGTATAATGAAGGTAAGCT
CAATATTACTGCTGCAATGAATGCTTTAAATAGTATTAAGCAAGCAGCACAGGAAGTTGCCCAGAAAAACTTACAA
AAGCAGTATGCTAAAAAAATTGAAAGAATAAGTTCAAAAGGATTAGCGTTATCTAAAAAGGCTAAAGAAATTTATG
AAAAGCATAAAAGTATTTTGCCTACACCTGGATATTATGCAGACTCTGTGGGAACTTATTTGAATAGGTTTAGAGA
TAAACAAACTTTCGGAAATAGGAGTGTTTGGACTGGTCAAAGTGGACTTGATGAAGCAAAAAAAATGCTTGATGAA
GTCAAAAAGCTTTTAAAAGAACTTCAAGACCTTACCAGAGGTACTAAAGAAGATAAAAAACCAGACGTTAAGCCAG
AAGCCAAACCAGAGGCCAAACCAGACGTTAAGCCAGAGGCCAAACCAGACGTTAAGCCAGAAGCTAAGCCAGACGT
TAAACCAGAAGCTAAGCCAGACGTTAAACCAGAAGCTAAGCCAGACGTTAAACCAGAAGCTAAGCCAGACGTTAAA
CCAAAGGCCAAACCAGACGTTAAGCCAGAAGCTAAGCCAGACGTTAAACCAGACGTTAAACCAGACGTTAAGCCAG
AGGCCAAACCAGAGGATAAGCCAGACGTTAAACCAGACGTTAAGCCAGAAGCTAAACCAGACGTTAAGCCAGAGGC
CAAACCAGAAGCTAAGCCAGAAGCTAAGCCAGAAGCTAAGCCAGAGGCCAAACCAGAAGCTAAGCCAGACGTTAAG
CCAGAAGCTAAACCAGACGTTAAACCAGAGGCTAAGCCAGAAGCTAAACCAGAGGCTAAGTCAGAAGCTAAACCAG
AGGCTAAGCTAGAAGCTAAACCAGAGGCCAAACCAGCAACCAAAAAATCGGTTAATACTAGCGGAAACTTGGCGGC
TAAAAAAGCTATTGAAAACAAAAAGTATAGTAAAAAATTACCATCAACGGGTGAAGCCGCAAGTCCACTCTTAGCA

ATTGTATCACTAATTGTTATGTTAAGTGCAGGTCTTATTACGATAGTTTTAAAGCATAAAAAAAAT

[86] Other embodiments of the invention provide nucleic acid molecules which encode a proline-rich domain of a BibA polypeptide. An example of such a nucleic acid molecule is set forth below as SEQ ID NO:17:

CCAGACGTTAAGCCAGAAGCCAAACCAGAGGCCAAACCAGACGTTAAGCCAGAGGCCAAACCAGACGTTAAGCCAGA
AGCTAAGCCAGACGTTAAACCAGAAGCTAAGCCAGACGTTAAACCAGAAGCTAAGCCAGACGTTAAACCAGAAGCTA
AGCCAGACGTTAAACCAAAGGCCAAACCAGACGTTAAGCCAGAAGCTAAGCCAGACGTTAAACCAGACGTTAAACCA
GACGTTAAGCCAGAGGCCAAACCAGAGGATAAGCCAGACGTTAAACCAGACGTTAAGCCAGAAGCTAAACCAGACGT
TAAGCCAGAGGCCAAACCAGAAGCTAAGCCAGAAGCTAAGCCAGAAGCTAAGCCAGAGGCCAAACCAGAAGCTAAGC
CAGACGTTAAGCCAGAAGCTAAACCAGACGTTAAACCAGAGGCTAAGCCAGAAGCTAAACCAGAGGCTAAGTCAGAA
GCTAAACCAGAGGCTAAGCTAGAAGCTAAACCAGAGGCCAAACCAGCAACCAAAAAATCGGTTAATACTAGCGGAAA
CTTGGCGGCTAAAAAAGCTATTGAAAACAAAAAGTATAGTAAAAAA

[87] A nucleic acid molecule encoding a highly conserved coiled-coil domain and proline-rich domain of a BibA polypeptide is set forth below as SEQ ID NO:18:

GGTATTGTACACGCGGATACTAGTTCAGGAATATCGGCTTCAATTCCTCATAAGAAACAAGTTAATTTAGGGGCGGT
TACTCTGAAGAATTTGATTTCTAAATATCGTGGTAATGACAAAGCTATTGCTATACTTTTAAGTAGAGTAAATGATT
TTAATAGAGCATCACAGGATACACTTCCACAATTAATTAATAGTACTGAAGCAGAAATTAGAAATATTTTATATCAA
GGACAAATTGGTAAGCAAAATAAACCAAGTGTAACTACACATGCTAAAGTTAGTGATCAAGAACTAGGTAAGCAGTC
AAGACGTTCTCAAGATATCATTAAGTCATTAGGTTTCCTTTCATCAGACCAAAAAGATATTTTAGTTAAATCTATTA
GCTCTTCAAAAGATTCGCAACTTATTCTTAAATTTGTAACTCAAGCCACGCAACTGAATAATGCTGAATCAACAAAA
GCTAAGCAAATGGCTCAAAATGACGTGGCCTTAATAAAAAATATAAGCCCCGAAGTCTTAGAAGAATATAAAGAAAA
AATTCAAAGAGCTAGCACTAAGAGTCAAGTTGATGAGTTTGTAGCAGAAGCTAAAAAAGTTGTTAATTCCAATAAAG
AAACGTTGGTAAATCAGGCCAATGGTAAAAAGCAAGAAATTGCTAAGTTAGAAAATTTATCTAACGATGAAATGTTG
AGATATAATACTGCAATTGATAATGTAGTGAAACAGTATAATGAAGGTAAGCTCAATATTACTGCTGCAATGAATGC
TTTAAATAGTATTAAGCAAGCAGCACAGGAAGTTGCCCAGAAAAACTTACAAAAGCAGTATGCTAAAAAAATTGAAA
GAATAAGTTCAAAAGGATTAGCGTTATCTAAAAAGGCTAAAGAAATTTATGAAAAGCATAAAAGTATTTTGCCTACA
CCTGGATATTATGCAGACTCTGTGGGAACTTATTTGAATAGGTTTAGAGATAAACAAACTTTCGGAAATAGGAGTGT
TTGGACTGGTCAAAGTGGACTTGATGAAGCAAAAAAAATGCTTGATGAAGTCAAAAAGCTTTTAAAAGAACTTCAAG
ACCTTACCAGAGGTACTAAAGAAGATAAAAAACCAGACGTTAAGCCAGAAGCCAAACCAGAGGCCAAACCAGACGTT
AAGCCAGAGGCCAAACCAGACGTTAAGCCAGAAGCTAAGCCAGACGTTAAACCAGAAGCTAAGCCAGACGTTAAACC
AGAAGCTAAGCCAGACGTTAAACCAGAAGCTAAGCCAGACGTTAAACCAAAGGCCAAACCAGACGTTAAGCCAGAAG
CTAAGCCAGACGTTAAACCAGACGTTAAACCAGACGTTAAGCCAGAGGCCAAACCAGAGGATAAGCCAGACGTTAAA
CCAGACGTTAAGCCAGAAGCTAAA

[88] A nucleic acid molecule which encodes a cell wall anchor of BibA is set forth as SEQ ID NO:19: TTACCATCAACGGGT.

III. Preparation of nucleic acid molecules

[89] Nucleic acid molecules of the invention can be prepared in many ways, for example, by chemical synthesis, from genomic or cDNA libraries (*e.g.*, using primer-based amplification methods, such as PCR), from the organism itself, *etc.*) and can take various forms (*e.g.* single-stranded, double-stranded, vectors, probes, *etc.*). They are preferably prepared in substantially pure form (*i.e.* substantially free from other GBS or host cell nucleic acids).

[90] Nucleic acid molecules can be synthesized, in whole or in part, using chemical methods well known in the art. See Caruthers *et al.*, *Nucl. Acids Res. Symp. Ser.* 215-223, 1980; Horn *et al. Nucl. Acids Res. Symp. Ser.* 225-232, 1980; Hunkapiller *et al.* (1984), Nature 310: 105-111; Grantham *et al.* (1981), Nucleic Acids Res. 9: r43-r74.

[91] cDNA molecules can be made with standard molecular biology techniques, using mRNA as a template. cDNA molecules can thereafter be replicated using molecular biology techniques well known in the art. An amplification technique, such as PCR, can be used to obtain additional copies of polynucleotides of the invention, using either genomic DNA or cDNA as a template.

[92] If desired, nucleotide sequences can be engineered using methods generally known in the art to alter coding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the polypeptide or mRNA product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides can be used to engineer the nucleotide sequences. For example, site-directed mutagenesis can be used to insert new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, introduce mutations, and so forth.

[93] Sequence modifications, such as the addition of a purification tag sequence or codon optimization, can be used to facilitate expression. For example, the N-terminal leader

sequence may be replaced with a sequence encoding for a tag protein such as polyhistidine ("HIS") or glutathione S-transferase ("GST"). Such tag proteins may be used to facilitate purification, detection, and stability of the expressed protein. Codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce an RNA transcript having desirable properties, such as a half-life which is longer than that of a transcript generated from the naturally occurring sequence. These methods are well known in the art and are further described in WO05/032582.

IV. Production of BibA polypeptides

[94] BibA polypeptides can be produced recombinantly, for example, by culturing a host cell transformed with nucleic acid molecules of the invention under conditions which permit polypeptide expression. BibA polypeptides can be synthesized by chemical means, or can be prepared from full-length BibA protein isolated from *S. agalactiae*.

A. Recombinant production of polypeptides

1. Nucleic acid molecules

[95] Any nucleic acid molecule which encodes a particular BibA polypeptide can be used to produce that polypeptide recombinantly. Recombinant production of BibA polypeptides can be facilitated by adding a nucleotide sequence encoding a tag protein in frame to the nucleotide sequence encoding the BibA polypeptide such that the polypeptide is expressed as a fusion protein comprising the tag protein and the GBS polypeptide. Such tag proteins can facilitate purification, detection, and stability of the expressed protein. Tag proteins suitable for use in the invention include a polyarginine tag (Arg-tag), polyhistidine tag (His-tag), FLAG-tag, Strep-tag, c-myc-tag, S-tag, calmodulin-binding peptide, cellulose-binding domain, SBP-tag,, chitin-binding domain, glutathione S-transferase-tag (GST), maltose-binding protein, transcription termination anti-termination factor (NusA), *E. coli* thioredoxin (TrxA), and protein disulfide isomerase I (DsbA).

Preferred tag proteins include His-tag and GST. See *Terpe et al.*, Appl Microbiol Biotechnol (2003) 60:523 – 33.

[96] After purification, a tag protein may optionally be removed from the expressed fusion protein, *i.e.*, by specifically tailored enzymatic treatments known in the art. Commonly used proteases include enterokinase, tobacco etch virus (TEV), thrombin, and factor X_a.

2. Expression constructs

[97] A nucleic acid molecule which encodes a polypeptide can be inserted into an expression construct which contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods which are well known to those skilled in the art can be used to construct expression constructs containing coding sequences and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination.

3. Host cells

[98] The heterologous host can be prokaryotic or eukaryotic. *E. coli* is a preferred host cell, but other suitable hosts include *Bacillus subtilis, Vibrio cholerae, Salmonella typhi, Salmonella typhimurium, Neisseria lactamica, Neisseria cinerea, Mycobacteria* (*e.g., M. tuberculosis*), yeasts, *etc.*

[99] A host cell strain can be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed polypeptide in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the polypeptide also can be used to facilitate correct insertion, folding and/or function. Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities are available from the American Type Culture Collection (ATCC; 10801

University Boulevard, Manassas, VA 20110-2209) and can be chosen to ensure the correct modification and processing of a foreign protein. See WO 01/98340.

[100] Expression constructs can be introduced into host cells using well-established techniques which include, but are not limited to, transferrin-polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-mediated cellular fusion, intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation, "gene gun" methods, and DEAE- or calcium phosphate-mediated transfection.

[101] Host cells transformed with expression constructs can be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell can be secreted or contained intracellularly depending on the nucleotide sequence and/or the expression construct used. Those of skill in the art understand that expression constructs can be designed to contain signal sequences which direct secretion of soluble polypeptides through a prokaryotic or eukaryotic cell membrane.

B. Purification

[102] BibA polypeptides of the invention can be isolated from the appropriate *Streptococcus agalactiae* bacterium or from an engineered host cell. A purified BibA polypeptide is separated from other components in the cell, such as proteins, carbohydrates, or lipids, using methods well-known in the art. Such methods include, but are not limited to, size exclusion chromatography, ammonium sulfate fractionation, ion exchange chromatography, affinity chromatography, and preparative gel electrophoresis. A preparation of purified BibA polypeptide is at least 80% pure; preferably, the preparations are 90%, 95%, or 99% pure. Purity of the preparations can be assessed by any means known in the art, such as SDS-polyacrylamide gel electrophoresis. Where appropriate, polypeptides can be solubilized, for example, with urea.

C. Chemical synthesis

[103] BibA polypeptides of the invention can be synthesized, for example, using solid-phase techniques. *See, e.g.*, Merrifield, *J. Am. Chem. Soc. 85*, 2149-54, 1963; Roberge *et al.*, *Science 269*, 202-04, 1995. Synthesis can be performed using manual techniques or by automation. Automated synthesis can be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer). Optionally, fragments of a polypeptide can be separately synthesized and combined using chemical methods to produce the final molecule.

V. Antibodies

[104] Antibodies can be generated to bind specifically to a BibA polypeptide or other antigen and can be used therapeutically and diagnostically. The term "antibody" includes intact immunoglobulin molecules, as well as fragments thereof which are capable of binding an antigen. These include hybrid (chimeric) antibody molecules (*e.g.*, Winter *et al.*, *Nature 349*, 293-99, 1991; U.S. Patent 4,816,567); $F(ab')_2$ and F(ab) fragments and F_v molecules; non-covalent heterodimers (*e.g.*, Inbar *et al.*, *Proc. Natl. Acad. Sci. U.S.A. 69*, 2659-62, 1972; Ehrlich *et al.*, *Biochem 19*, 4091-96, 1980); single-chain Fv molecules (sFv) (*e.g.*, Huston *et al.*, *Proc. Natl. Acad. Sci. U.S.A. 85*, 5897-83, 1988); dimeric and trimeric antibody fragment constructs; minibodies (*e.g.*, Pack *et al.*, *Biochem 31*, 1579-84, 1992; Cumber *et al.*, *J. Immunology 149B*, 120-26, 1992); humanized antibody molecules (*e.g.*, Riechmann *et al.*, *Nature 332*, 323-27, 1988; Verhoeyan *et al.*, *Science 239*, 1534-36, 1988; and U.K. Patent Publication No. GB 2,276,169, published 21 September 1994); and any functional fragments obtained from such molecules, as well as antibodies obtained through non-conventional processes such as phage display. Preferably, the antibodies are monoclonal antibodies. Methods of obtaining monoclonal antibodies are well known in the art.

[105] Preferred antibodies of the invention specifically bind to an epitope in the N-terminal domain, coiled-coil domain, or proline-rich domain of BibA. Typically, at least 6, 7, 8,

10, or 12 contiguous amino acids are required to form an epitope. However, epitopes which involve non-contiguous amino acids may require more, *e.g.*, at least 15, 25, or 50 amino acids. Various immunoassays (*e.g.*, Western blots, ELISAs, radioimmunoassays, immunohistochemical assays, immunoprecipitations, or other immunochemical assays known in the art) can be used to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric assays are well known in the art. Such immunoassays typically involve the measurement of complex formation between an immunogen and an antibody which specifically binds to the immunogen. A preparation of antibodies which specifically bind to a particular antigen typically provides a detection signal at least 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in an immunochemical assay. Preferably, the antibodies do not detect other proteins in immunochemical assays and can immunoprecipitate the particular antigen from solution.

[106] Polypeptides can be used to immunize a mammal, such as a mouse, rat, rabbit, guinea pig, monkey, or human, to produce polyclonal antibodies. If desired, an antigen can be conjugated to a carrier protein, such as bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin. Depending on the host species, various adjuvants can be used to increase the immunological response. Such adjuvants include, but are not limited to, Freund's adjuvant, mineral gels (*e.g.*, aluminum hydroxide), and surface active substances (*e.g.* lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanin, and dinitrophenol). Among adjuvants used in humans, BCG (*bacilli Calmette-Guerin*) and *Corynebacterium parvum* are especially useful.

[107] Monoclonal antibodies which specifically bind to an antigen can be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These techniques include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique (Kohler *et al.*, *Nature 256*, 495-497, 1985; Kozbor *et al.*, *J. Immunol. Methods 81*, 31-42,

1985; Cote *et al.*, *Proc. Natl. Acad. Sci. 80*, 2026-2030, 1983; Cole *et al.*, *Mol. Cell Biol. 62*, 109-120, 1984).

[108] In addition, techniques developed for the production of "chimeric antibodies," the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used (Morrison *et al.*, *Proc. Natl. Acad. Sci. 81*, 6851-6855, 1984; Neuberger *et al.*, *Nature 312*, 604-608, 1984; Takeda *et al.*, *Nature 314*, 452-454, 1985). Monoclonal and other antibodies also can be "humanized" to prevent a patient from mounting an immune response against the antibody when it is used therapeutically. Such antibodies may be sufficiently similar in sequence to human antibodies to be used directly in therapy or may require alteration of a few key residues. Sequence differences between rodent antibodies and human sequences can be minimized by replacing residues which differ from those in the human sequences by site directed mutagenesis of individual residues or by grating of entire complementarity determining regions.

[109] Alternatively, humanized antibodies can be produced using recombinant methods, as described below. Antibodies which specifically bind to a particular antigen can contain antigen binding sites which are either partially or fully humanized, as disclosed in U.S. 5,565,332.

[110] Alternatively, techniques described for the production of single chain antibodies can be adapted using methods known in the art to produce single chain antibodies which specifically bind to a particular antigen. Antibodies with related specificity, but of distinct idiotypic composition, can be generated by chain shuffling from random combinatorial immunoglobin libraries (Burton, *Proc. Natl. Acad. Sci. 88*, 11120-23, 1991).

[111] Single-chain antibodies also can be constructed using a DNA amplification method, such as PCR, using hybridoma cDNA as a template (Thirion *et al.*, 1996, *Eur. J. Cancer Prev. 5*, 507-11). Single-chain antibodies can be mono- or bispecific, and can be bivalent or

tetravalent. Construction of tetravalent, bispecific single-chain antibodies is taught, for example, in Coloma & Morrison, 1997, *Nat. Biotechnol. 15*, 159-63. Construction of bivalent, bispecific single-chain antibodies is taught in Mallender & Voss, 1994, *J. Biol. Chem. 269*, 199-206.

[112] A nucleotide sequence encoding a single-chain antibody can be constructed using manual or automated nucleotide synthesis, cloned into an expression construct using standard recombinant DNA methods, and introduced into a cell to express the coding sequence, as described below. Alternatively, single-chain antibodies can be produced directly using, for example, filamentous phage technology (Verhaar *et al.*, 1995, *Int. J. Cancer 61*, 497-501; Nicholls *et al.*, 1993, *J. Immunol. Meth. 165*, 81-91).

[113] Antibodies which specifically bind to a particular antigen also can be produced by inducing *in vivo* production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature (Orlandi *et al.*, *Proc. Natl. Acad. Sci. 86*, 3833-3837, 1989; Winter *et al.*, *Nature 349*, 293-299, 1991).

[114] Chimeric antibodies can be constructed as disclosed in WO 93/03151. Binding proteins which are derived from immunoglobulins and which are multivalent and multispecific, such as the "diabodies" described in WO 94/13804, also can be prepared.

[115] Antibodies can be purified by methods well known in the art. For example, antibodies can be affinity purified by passage over a column to which the relevant antigen is bound. The bound antibodies can then be eluted from the column using a buffer with a high salt concentration.

VI. Compositions comprising one or more active agents

[116] The invention provides compositions for preventing and for treating *S. agalactiae* infection. Compositions of the invention comprise at least one active agent. The active agent can be a BibA polypeptide, a nucleic acid molecule encoding a BibA polypeptide,

or antibodies which specifically bind to a BibA polypeptide. Suitable BibA polypeptides include, for example, those identified in groups "I," "II," and "III" in **FIG. 24.** Compositions of the invention can include one or more BibA polypeptides of two or more of these groups.

[117] Compositions of the invention can include one or more additional active agents. Such agents include, but are not limited to one or more (a) GBS antigens, (b) non-GBS antigens, (c) nucleic acid molecules encoding (a) or (b), and antibodies which specifically bind to (a) or (b).

A. GBS antigens

[118] GBS antigens which can be included in compositions of the invention include antigenic portions of the GBS proteins disclosed in WO 02/34771 (*e.g.*, GBS1-GBS689), which is incorporated herein by reference in its entirety. Preferred antigens include GBS 80, GBS 104, GBS 322, GBS 67, GBS 276, and GBS 59.

B. Non-GBS antigens

[119] Compositions of the invention may be administered in conjunction with one or more antigens for use in therapeutic, prophylactic, or diagnostic methods of the present invention. Compositions of the invention optionally can comprise one or more additional polypeptide antigens which are not derived from *S. agalactiae* proteins. Preferred antigens include those listed below. Additionally, the compositions of the present invention may be used to treat or prevent infections caused by any of the below-listed pathogens. In addition to combination with the antigens described below, the compositions of the invention may also be combined with an adjuvant as described herein.

[120] Antigens for use with the invention include, but are not limited to, one or more of the following antigens set forth below, or antigens derived from one or more of the pathogens set forth below:

1. Bacterial Antigens

[121] Bacterial antigens suitable for use in the invention include proteins, polysaccharides, lipopolysaccharides, and outer membrane vesicles which may be isolated, purified or derived from a bacteria. In addition, bacterial antigens may include bacterial lysates and inactivated bacteria formulations. Bacteria antigens may be produced by recombinant expression. Bacterial antigens preferably include epitopes which are exposed on the surface of the bacteria during at least one stage of its life cycle. Bacterial antigens are preferably conserved across multiple serotypes. Bacterial antigens include antigens derived from one or more of the bacteria set forth below as well as the specific antigens examples identified below.

[122] *Neisseria meningitides*: *Meningitides* antigens may include proteins (such as those identified in References 1 – 7), saccharides (including a polysaccharide, oligosaccharide or lipopolysaccharide), or outer-membrane vesicles (References 8, 9, 10, 11) purified or derived from *N. meningitides* serogroup such as A, C, W135, Y, and/or B. *Meningitides* protein antigens may be selected from adhesions, autotransporters, toxins, Fe acquisition proteins, and membrane associated proteins (preferably integral outer membrane protein).

[123] *Streptococcus pneumoniae*: *Streptococcus pneumoniae* antigens may include a saccharide (including a polysaccharide or an oligosaccharide) and/or protein from *Streptococcus pneumoniae*. Saccharide antigens may be selected from serotypes 1, 2, 3, 4, 5, 6B, 7F, 8, 9N, 9V, 10A, 11A, 12F, 14, 15B, 17F, 18C, 19A, 19F, 20, 22F, 23F, and 33F. Protein antigens may be selected from a protein identified in WO 98/18931, WO 98/18930, US Patent No. 6,699,703, US Patent No. 6,800,744, WO 97/43303, and WO 97/37026. *Streptococcus pneumoniae* proteins may be selected from the Poly Histidine Triad family (PhtX), the Choline Binding Protein family (CbpX), CbpX truncates, LytX family, LytX truncates, CbpX truncate-LytX truncate chimeric proteins, pneumolysin (Ply), PspA, PsaA, Sp128, Sp101, Sp130, Sp125 or Sp133.

[124] *Streptococcus pyogenes* (Group A Streptococcus): Group A *Streptococcus* antigens may include a protein identified in WO 02/34771 or WO 2005/032582 (including GBS 40), fusions of fragments of GBS M proteins (including those described in WO 02/094851, and Dale, Vaccine (1999) 17:193-200, and Dale, Vaccine 14(10): 944-948), fibronectin binding protein (Sfb1), Streptococcal heme-associated protein (Shp), and Streptolysin S (SagA).

[125] *Moraxella catarrhalis*: *Moraxella* antigens include antigens identified in WO 02/18595 and WO 99/58562, outer membrane protein antigens (HMW-OMP), C-antigen, and/or LPS.

[126] *Bordetella pertussis*: Pertussis antigens include pertussis holotoxin (PT) and filamentous haemagglutinin (FHA) from *B. pertussis*, optionally also combination with pertactin and/or agglutinogens 2 and 3 antigen.

[127] *Staphylococcus aureus*: *Staphylococcus aureus* antigens include *S. aureus* type 5 and 8 capsular polysaccharides optionally conjugated to nontoxic recombinant *Pseudomonas aeruginosa* exotoxin A, such as StaphVAX™, or antigens derived from surface proteins, invasins (leukocidin, kinases, hyaluronidase), surface factors that inhibit phagocytic engulfment (capsule, Protein A), carotenoids, catalase production, Protein A, coagulase, clotting factor, and/or membrane-damaging toxins (optionally detoxified) that lyse eukaryotic cell membranes (hemolysins, leukotoxin, leukocidin).

[128] *Staphylococcus epidermis*: *S. epidermidis* antigens include slime-associated antigen (SAA).

[129] *Clostridium tetani* (Tetanus): Tetanus antigens include tetanus toxoid (TT), preferably used as a carrier protein in conjunction/conjugated with the compositions of the present invention.

[130] *Cornynebacterium diphtheriae* (Diphtheria): Diphtheria antigens include diphtheria toxin, preferably detoxified, such as CRM197. Additionally antigens capable of modulating,

inhibiting or associated with ADP ribosylation are contemplated for combination/co-administration/conjugation with the compositions of the present invention. The diphtheria toxoids may be used as carrier proteins.

[131] *Haemophilus influenzae B* (Hib): Hib antigens include a Hib saccharide antigen.

[132] *Pseudomonas aeruginosa*: *Pseudomonas* antigens include endotoxin A, Wzz protein, P. aeruginosa LPS, more particularly LPS isolated from PAO1 (O5 serotype), and/or Outer Membrane Proteins, including Outer Membrane Proteins F (OprF) (Infect Immun. 2001 May; 69(5): 3510-3515).

[133] *Legionella pneumophila.* Bacterial antigens may be derived from *Legionella pneumophila.*

[134] *Streptococcus agalactiae* (Group B Streptococcus): Group B *Streptococcus* antigens include a protein or saccharide antigen identified in WO 02/34771, WO 03/093306, WO 04/041157, or WO 2005/002619 (including proteins GBS 80, GBS 104, GBS 276 and GBS 322, and including saccharide antigens derived from serotypes Ia, Ib, Ia/c, II, III, IV, V, VI, VII and VIII).

[135] *Neiserria gonorrhoeae*: *Gonorrhoeae* antigens include Por (or porin) protein, such as PorB (see Zhu et al., Vaccine (2004) 22:660 – 669), a transferring binding protein, such as TbpA and TbpB (See Price et al., Infection and Immunity (2004) 71(1):277 – 283), a opacity protein (such as Opa), a reduction-modifiable protein (Rmp), and outer membrane vesicle (OMV) preparations (see Plante et al., J Infectious Disease (2000) 182:848 – 855), also see e.g. WO99/24578, WO99/36544, WO99/57280, WO02/079243).

[136] *Chlamydia trachomatis*: *Chlamydia trachomatis* antigens include antigens derived from serotypes A, B, Ba and C (agents of trachoma, a cause of blindness), serotypes L1, L2 & L3 (associated with *Lymphogranuloma venereum*), and serotypes, D-K. Chlamydia trachomas antigens may also include an antigen identified in WO 00/37494, WO

03/049762, WO 03/068811, or WO 05/002619, including PepA (CT045), LcrE (CT089), ArtJ (CT381), DnaK (CT396), CT398, OmpH-like (CT242), L7/L12 (CT316), OmcA (CT444), AtosS (CT467), CT547, Eno (CT587), HrtA (CT823), and MurG (CT761).

[137] *Treponema pallidum* (Syphilis): Syphilis antigens include TmpA antigen.

[138] *Haemophilus ducreyi* (causing chancroid): Ducreyi antigens include outer membrane protein (DsrA).

[139] *Enterococcus faecalis* or *Enterococcus faecium*: Antigens include a trisaccharide repeat or other *Enterococcus* derived antigens provided in US Patent No. 6,756,361.

[140] *Helicobacter pylori*: *H. pylori* antigens include Cag, Vac, Nap, HopX, HopY and/or urease antigen.

[141] *Staphylococcus saprophyticus*: Antigens include the 160 kDa hemagglutinin of *S. saprophyticus* antigen.

[142] *Yersinia enterocolitica* antigens include LPS (Infect Immun. 2002 August; 70(8): 4414).

[143] *E. coli*: *E. coli* antigens may be derived from enterotoxigenic *E. coli* (ETEC), enteroaggregative *E. coli* (EAggEC), diffusely adhering *E. coli* (DAEC), enteropathogenic *E. coli* (EPEC), and/or enterohemorrhagic *E. coli* (EHEC).

[144] *Bacillus anthracis* (anthrax): *B. anthracis* antigens are optionally detoxified and may be selected from A-components (lethal factor (LF) and edema factor (EF)), both of which can share a common B-component known as protective antigen (PA).

[145] *Yersinia pestis* (plague): Plague antigens include F1 capsular antigen (Infect Immun. 2003 Jan; 71(1)): 374-383, LPS (Infect Immun. 1999 Oct; 67(10): 5395), *Yersinia pestis* V antigen (Infect Immun. 1997 Nov; 65(11): 4476-4482).

[146] *Mycobacterium tuberculosis*: Tuberculosis antigens include lipoproteins, LPS, BCG antigens, a fusion protein of antigen 85B (Ag85B) and/or ESAT-6 optionally formulated in cationic lipid vesicles (Infect Immun. 2004 October; 72(10): 6148), *Mycobacterium tuberculosis* (Mtb) isocitrate dehydrogenase associated antigens (Proc Natl Acad Sci U S A. 2004 Aug 24; 101(34): 12652), and/or MPT51 antigens (Infect Immun. 2004 July; 72(7): 3829).

[147] *Rickettsia*: Antigens include outer membrane proteins, including the outer membrane protein A and/or B (OmpB) (Biochim Biophys Acta. 2004 Nov 1;1702(2):145), LPS, and surface protein antigen (SPA) (J Autoimmun. 1989 Jun;2 Suppl:81).

[148] *Listeria monocytogenes*. Bacterial antigens may be derived from Listeria monocytogenes.

[149] *Chlamydia pneumoniae*: Antigens include those identified in WO 02/02606.

[150] *Vibrio cholerae*: Antigens include proteinase antigens, LPS, particularly lipopolysaccharides of *Vibrio cholerae* II, O1 Inaba O-specific polysaccharides, V. cholera O139, antigens of IEM108 vaccine (Infect Immun. 2003 Oct;71(10):5498-504), and/or Zonula occludens toxin (Zot).

[151] *Salmonella typhi* (typhoid fever): Antigens include capsular polysaccharides preferably conjugates (Vi, i.e. vax-TyVi).

[152] *Borrelia burgdorferi* (Lyme disease): Antigens include lipoproteins (such as OspA, OspB, Osp C and Osp D), other surface proteins such as OspE-related proteins (Erps), decorin-binding proteins (such as DbpA), and antigenically variable VI proteins. , such as antigens associated with P39 and P13 (an integral membrane protein, Infect Immun. 2001 May; 69(5): 3323-3334), VlsE Antigenic Variation Protein (J Clin Microbiol. 1999 Dec; 37(12): 3997).

[153] *Porphyromonas gingivalis*: Antigens include *P. gingivalis* outer membrane protein (OMP).

[154] *Klebsiella*: Antigens include an OMP, including OMP A, or a polysaccharide optionally conjugated to tetanus toxoid.

[155] Further bacterial antigens of the invention may be capsular antigens, polysaccharide antigens or protein antigens of any of the above. Further bacterial antigens may also include an outer membrane vesicle (OMV) preparation. Additionally, antigens include live, attenuated, and/or purified versions of any of the aforementioned bacteria. The antigens of the present invention may be derived from gram-negative or gram-positive bacteria. The antigens of the present invention may be derived from aerobic or anaerobic bacteria.

[156] Additionally, any of the above bacterial-derived saccharides (polysaccharides, LPS, LOS or oligosaccharides) can be conjugated to another agent or antigen, such as a carrier protein (for example CRM197). Such conjugation may be direct conjugation effected by reductive amination of carbonyl moieties on the saccharide to amino groups on the protein, as provided in US Patent No. 5,360,897 and Can J Biochem Cell Biol. 1984 May;62(5):270-5. Alternatively, the saccharides can be conjugated through a linker, such as, with succinamide or other linkages provided in Bioconjugate Techniques, 1996 and CRC, Chemistry of Protein Conjugation and Cross-Linking, 1993.

2. Viral Antigens

[157] Viral antigens suitable for use in the invention include inactivated (or killed) virus, attenuated virus, split virus formulations, purified subunit formulations, viral proteins which may be isolated, purified or derived from a virus, and Virus Like Particles (VLPs). Viral antigens may be derived from viruses propagated on cell culture or other substrate. Alternatively, viral antigens may be expressed recombinantly. Viral antigens preferably include epitopes which are exposed on the surface of the virus during at least one stage of

its life cycle. Viral antigens are preferably conserved across multiple serotypes or isolates. Viral antigens include antigens derived from one or more of the viruses set forth below as well as the specific antigens examples identified below.

[158] *Orthomyxovirus*: Viral antigens may be derived from an *Orthomyxovirus*, such as Influenza A, B and C. *Orthomyxovirus* antigens may be selected from one or more of the viral proteins, including hemagglutinin (HA), neuraminidase (NA), nucleoprotein (NP), matrix protein (M1), membrane protein (M2), one or more of the transcriptase components (PB1, PB2 and PA). Preferred antigens include HA and NA.

[159] Influenza antigens may be derived from interpandemic (annual) flu strains. Alternatively influenza antigens may be derived from strains with the potential to cause pandemic a pandemic outbreak (i.e., influenza strains with new haemagglutinin compared to the haemagglutinin in currently circulating strains, or influenza strains which are pathogenic in avian subjects and have the potential to be transmitted horizontally in the human population, or influenza strains which are pathogenic to humans).

[160] Paramyxoviridae viruses: Viral antigens may be derived from Paramyxoviridae viruses, such as Pneumoviruses (RSV), Paramyxoviruses (PIV) and Morbilliviruses (Measles).

[161] Pneumovirus: Viral antigens may be derived from a Pneumovirus, such as Respiratory syncytial virus (RSV), Bovine respiratory syncytial virus, Pneumonia virus of mice, and Turkey rhinotracheitis virus. Preferably, the Pneumovirus is RSV. Pneumovirus antigens may be selected from one or more of the following proteins, including surface proteins Fusion (F), Glycoprotein (G) and Small Hydrophobic protein (SH), matrix proteins M and M2, nucleocapsid proteins N, P and L and nonstructural proteins NS1 and NS2. Preferred Pneumovirus antigens include F, G and M. See e.g., J Gen Virol. 2004 Nov; 85(Pt 11):3229). Pneumovirus antigens may also be formulated in or derived from chimeric viruses. For example, chimeric RSV/PIV viruses may comprise components of both RSV and PIV.

[162] Paramyxovirus: Viral antigens may be derived from a Paramyxovirus, such as Parainfluenza virus types 1 – 4 (PIV), Mumps, Sendai viruses, Simian virus 5, Bovine parainfluenza virus and Newcastle disease virus. Preferably, the Paramyxovirus is PIV or Mumps. Paramyxovirus antigens may be selected from one or more of the following proteins: Hemagglutinin –Neuraminidase (HN), Fusion proteins F1 and F2, Nucleoprotein (NP), Phosphoprotein (P), Large protein (L), and Matrix protein (M). Preferred Paramyxovirus proteins include HN, F1 and F2. Paramyxovirus antigens may also be formulated in or derived from chimeric viruses. For example, chimeric RSV/PIV viruses may comprise components of both RSV and PIV. Commercially available mumps vaccines include live attenuated mumps virus, in either a monovalent form or in combination with measles and rubella vaccines (MMR).

[163] Morbillivirus: Viral antigens may be derived from a Morbillivirus, such as Measles. Morbillivirus antigens may be selected from one or more of the following proteins: hemagglutinin (H), Glycoprotein (G), Fusion factor (F), Large protein (L), Nucleoprotein (NP), Polymerase phosphoprotein (P), and Matrix (M). Commercially available measles vaccines include live attenuated measles virus, typically in combination with mumps and rubella (MMR).

[164] Picornavirus: Viral antigens may be derived from Picornaviruses, such as Enteroviruses, Rhinoviruses, Heparnavirus, Cardioviruses and Aphthoviruses. Antigens derived from Enteroviruses, such as Poliovirus are preferred.

[165] Enterovirus: Viral antigens may be derived from an Enterovirus, such as Poliovirus types 1, 2 or 3, Coxsackie A virus types 1 to 22 and 24, Coxsackie B virus types 1 to 6, Echovirus (ECHO) virus) types 1 to 9, 11 to 27 and 29 to 34 and Enterovirus 68 to 71. Preferably, the Enterovirus is poliovirus. Enterovirus antigens are preferably selected from one or more of the following Capsid proteins VP1, VP2, VP3 and VP4. Commercially available polio vaccines include Inactivated Polio Vaccine (IPV) and Oral poliovirus vaccine (OPV).

[166] Heparnavirus: Viral antigens may be derived from an Heparnavirus, such as Hepatitis A virus (HAV). Commercially available HAV vaccines include inactivated HAV vaccine.

[167] Togavirus: Viral antigens may be derived from a Togavirus, such as a Rubivirus, an Alphavirus, or an Arterivirus. Antigens derived from Rubivirus, such as Rubella virus, are preferred. Togavirus antigens may be selected from E1, E2, E3, C, NSP-1, NSPO-2, NSP-3 or NSP-4. Togavirus antigens are preferably selected from E1, E2 or E3. Commercially available Rubella vaccines include a live cold-adapted virus, typically in combination with mumps and measles vaccines (MMR).

[168] Flavivirus: Viral antigens may be derived from a Flavivirus, such as Tick-borne encephalitis (TBE), Dengue (types 1, 2, 3 or 4), Yellow Fever, Japanese encephalitis, West Nile encephalitis, St. Louis encephalitis, Russian spring-summer encephalitis, Powassan encephalitis. Flavivirus antigens may be selected from PrM, M, C, E, NS-1, NS-2a, NS2b, NS3, NS4a, NS4b, and NS5. Flavivirus antigens are preferably selected from PrM, M and E. Commercially available TBE vaccine include inactivated virus vaccines.

[169] Pestivirus: Viral antigens may be derived from a Pestivirus, such as Bovine viral diarrhea (BVDV), Classical swine fever (CSFV) or Border disease (BDV).

[170] Hepadnavirus: Viral antigens may be derived from a Hepadnavirus, such as Hepatitis B virus. Hepadnavirus antigens may be selected from surface antigens (L, M and S), core antigens (HBc, HBe). Commercially available HBV vaccines include subunit vaccines comprising the surface antigen S protein.

[171] Hepatitis C virus: Viral antigens may be derived from a Hepatitis C virus (HCV). HCV antigens may be selected from one or more of E1, E2, E1/E2, NS345 polyprotein, NS 345-core polyprotein, core, and/or peptides from the nonstructural regions (Houghton et al., Hepatology (1991) 14:381).

[172] Rhabdovirus: Viral antigens may be derived from a Rhabdovirus, such as a Lyssavirus (Rabies virus) and Vesiculovirus (VSV). Rhabdovirus antigens may be selected from glycoprotein (G), nucleoprotein (N), large protein (L), nonstructural proteins (NS). Commercially available Rabies virus vaccine comprise killed virus grown on human diploid cells or fetal rhesus lung cells.

[173] Caliciviridae; Viral antigens may be derived from Calciviridae, such as Norwalk virus, and Norwalk-like Viruses, such as Hawaii Virus and Snow Mountain Virus.

[174] Coronavirus: Viral antigens may be derived from a Coronavirus, SARS, Human respiratory coronavirus, Avian infectious bronchitis (IBV), Mouse hepatitis virus (MHV), and Porcine transmissible Gastroenteritis virus (TGEV). Coronavirus antigens may be selected from spike (S), envelope (E), matrix (M), nucleocapsid (N), and Hemagglutinin-esterase glycoprotein (HE). Preferably, the Coronavirus antigen is derived from a SARS virus. SARS viral antigens are described in WO 04/92360;

[175] Retrovirus: Viral antigens may be derived from a Retrovirus, such as an Oncovirus, a Lentivirus or a Spumavirus. Oncovirus antigens may be derived from HTLV-1, HTLV-2 or HTLV-5. Lentivirus antigens may be derived from HIV-1 or HIV-2. Retrovirus antigens may be selected from gag, pol, env, tax, tat, rex, rev, nef, vif, vpu, and vpr. HIV antigens may be selected from gag (p24gag and p55gag), env (gp160 and gp41), pol, tat, nef, rev vpu, miniproteins, (preferably p55 gag and gp140v delete). HIV antigens may be derived from one or more of the following strains: HIVIIIb, HIVSF2, HIVLAV, HIVLAI, HIVMN, HIV-1CM235, HIV-1US4.

[176] Reovirus: Viral antigens may be derived from a Reovirus, such as an Orthoreovirus, a Rotavirus, an Orbivirus, or a Coltivirus. Reovirus antigens may be selected from structural proteins λ1, λ2, λ3, μ1, μ2, σ1, σ2, or σ3, or nonstructural proteins σNS, μNS, or σ1s. Preferred Reovirus antigens may be derived from a Rotavirus. Rotavirus antigens may be selected from VP1, VP2, VP3, VP4 (or the cleaved product VP5 and

VP8), NSP 1, VP6, NSP3, NSP2, VP7, NSP4, or NSP5. Preferred Rotavirus antigens include VP4 (or the cleaved product VP5 and VP8), and VP7.

[177] Parvovirus: Viral antigens may be derived from a Parvovirus, such as Parvovirus B19. Parvovirus antigens may be selected from VP-1, VP-2, VP-3, NS-1 and NS-2. Preferably, the Parvovirus antigen is capsid protein VP-2.

[178] Delta hepatitis virus (HDV): Viral antigens may be derived HDV, particularly δ-antigen from HDV (see, e.g., U.S. Patent No. 5,378,814).

[179] Hepatitis E virus (HEV): Viral antigens may be derived from HEV.

[180] Hepatitis G virus (HGV): Viral antigens may be derived from HGV.

[181] Human Herpesvirus: Viral antigens may be derived from a Human Herpesvirus, such as Herpes Simplex Viruses (HSV), Varicella-zoster virus (VZV), Epstein-Barr virus (EBV), Cytomegalovirus (CMV), Human Herpesvirus 6 (HHV6), Human Herpesvirus 7 (HHV7), and Human Herpesvirus 8 (HHV8). Human Herpesvirus antigens may be selected from immediate early proteins (α), early proteins (β), and late proteins (γ). HSV antigens may be derived from HSV-1 or HSV-2 strains. HSV antigens may be selected from glycoproteins gB, gC, gD and gH, fusion protein (gB), or immune escape proteins (gC, gE, or gI). VZV antigens may be selected from core, nucleocapsid, tegument, or envelope proteins. A live attenuated VZV vaccine is commercially available. EBV antigens may be selected from early antigen (EA) proteins, viral capsid antigen (VCA), and glycoproteins of the membrane antigen (MA). CMV antigens may be selected from capsid proteins, envelope glycoproteins (such as gB and gH), and tegument proteins

[182] Papovaviruses: Antigens may be derived from Papovaviruses, such as Papillomaviruses and Polyomaviruses. Papillomaviruses include HPV serotypes 1, 2, 4, 5, 6, 8, 11, 13, 16, 18, 31, 33, 35, 39, 41, 42, 47, 51, 57, 58, 63 and 65. Preferably, HPV antigens are derived from serotypes 6, 11, 16 or 18. HPV antigens may be selected from capsid proteins (L1) and (L2), or E1 – E7, or fusions thereof. HPV antigens are preferably

formulated into virus-like particles (VLPs). Polyomyavirus viruses include BK virus and JK virus. Polyomavirus antigens may be selected from VP1, VP2 or VP3.

[183] Further provided are antigens, compositions, methods, and microbes included in Vaccines, 4th Edition (Plotkin and Orenstein ed. 2004); Medical Microbiology 4th Edition (Murray et al. ed. 2002); Virology, 3rd Edition (W.K. Joklik ed. 1988); Fundamental Virology, 2nd Edition (B.N. Fields and D.M. Knipe, eds. 1991), which are contemplated in conjunction with the compositions of the present invention.

3. Fungal Antigens

[184] Fungal antigens for use in the invention may be derived from one or more of the fungi set forth below.

[185] Fungal antigens may be derived from Dermatophytres, including: Epidermophyton floccusum, Microsporum audouini, Microsporum canis, Microsporum distortum, Microsporum equinum, Microsporum gypsum, Microsporum nanum, Trichophyton concentricum, Trichophyton equinum, Trichophyton gallinae, Trichophyton gypseum, Trichophyton megnini, Trichophyton mentagrophytes, Trichophyton quinckeanum, Trichophyton rubrum, Trichophyton schoenleini, Trichophyton tonsurans, Trichophyton verrucosum, T. verrucosum var. album, var. discoides, var. ochraceum, Trichophyton violaceum, and/or Trichophyton faviforme.

[186] Fungal pathogens may be derived from Aspergillus fumigatus, Aspergillus flavus, Aspergillus niger, Aspergillus nidulans, Aspergillus terreus, Aspergillus sydowi, Aspergillus flavatus, Aspergillus glaucus, Blastoschizomyces capitatus, Candida albicans, Candida enolase, Candida tropicalis, Candida glabrata, Candida krusei, Candida parapsilosis, Candida stellatoidea, Candida kusei, Candida parakwsei, Candida lusitaniae, Candida pseudotropicalis, Candida guilliermondi, Cladosporium carrionii, Coccidioides immitis, Blastomyces dermatidis, Cryptococcus neoformans, Geotrichum clavatum, Histoplasma capsulatum, Klebsiella pneumoniae, Paracoccidioides brasiliensis,

Pneumocystis carinii, Pythiumn insidiosum, Pityrosporum ovale, Sacharomyces cerevisae, Saccharomyces boulardii, Saccharomyces pombe, Scedosporium apiosperum, Sporothrix schenckii, Trichosporon beigelii, Toxoplasma gondii, Penicillium marneffei, Malassezia spp., Fonsecaea spp., Wangiella spp., Sporothrix spp., Basidiobolus spp., Conidiobolus spp., Rhizopus spp, Mucor spp, Absidia spp, Mortierella spp, Cunninghamella spp, Saksenaea spp., Alternaria spp, Curvularia spp, Helminthosporium spp, Fusarium spp, Aspergillus spp, Penicillium spp, Monolinia spp, Rhizoctonia spp, Paecilomyces spp, Pithomyces spp, and Cladosporium spp.

[187] Processes for producing a fungal antigens are well known in the art (see US Patent No. 6,333,164). In a preferred method a solubilized fraction extracted and separated from an insoluble fraction obtainable from fungal cells of which cell wall has been substantially removed or at least partially removed, characterized in that the process comprises the steps of: obtaining living fungal cells; obtaining fungal cells of which cell wall has been substantially removed or at least partially removed; bursting the fungal cells of which cell wall has been substantially removed or at least partially removed; obtaining an insoluble fraction; and extracting and separating a solubilized fraction from the insoluble fraction.

4. STD Antigens

[188] The compositions of the invention may include one or more antigens derived from a sexually transmitted disease (STD). Such antigens may provide for prophylactis or therapy for STD's such as chlamydia, genital herpes, hepatitis (such as HCV), genital warts, gonorrhoea, syphilis and/or chancroid (See, WO00/15255). Antigens may be derived from one or more viral or bacterial STD's. Viral STD antigens for use in the invention may be derived from, for example, HIV, herpes simplex virus (HSV-1 and HSV-2), human papillomavirus (HPV), and hepatitis (HCV). Bacterial STD antigens for use in the invention may be derived from, for example, Neiserria gonorrhoeae, Chlamydia trachomatis, Treponema pallidum, Haemophilus ducreyi, E. coli, and

Streptococcus agalactiae. Examples of specific antigens derived from these pathogens are described above.

5. Respiratory Antigens

[189] The compositions of the invention may include one or more antigens derived from a pathogen which causes respiratory disease. For example, respiratory antigens may be derived from a respiratory virus such as Orthomyxoviruses (influenza), Pneumovirus (RSV), Paramyxovirus (PIV), Morbillivirus (measles), Togavirus (Rubella), VZV, and Coronavirus (SARS). Respiratory antigens may be derived from a bacteria which causes respiratory disease, such as Streptococcus pneumoniae, Pseudomonas aeruginosa, Bordetella pertussis, Mycobacterium tuberculosis, Mycoplasma pneumoniae, Chlamydia pneumoniae, Bacillus anthracis, and Moraxella catarrhalis. Examples of specific antigens derived from these pathogens are described above.

6. Pediatric Vaccine Antigens

[190] The compositions of the invention may include one or more antigens suitable for use in pediatric subjects. Pediatric subjects are typically less than about 3 years old, or less than about 2 years old, or less than about 1 years old. Pediatric antigens may be administered multiple times over the course of 6 months, 1, 2 or 3 years. Pediatric antigens may be derived from a virus which may target pediatric populations and/or a virus from which pediatric populations are susceptible to infection. Pediatric viral antigens include antigens derived from one or more of Orthomyxovirus (influenza), Pneumovirus (RSV), Paramyxovirus (PIV and Mumps), Morbillivirus (measles), Togavirus (Rubella), Enterovirus (polio), HBV, Coronavirus (SARS), and Varicella-zoster virus (VZV), Epstein Barr virus (EBV). Pediatric bacterial antigens include antigens derived from one or more of Streptococcus pneumoniae, Neisseria meningitides, Streptococcus pyogenes (Group A Streptococcus), Moraxella catarrhalis, Bordetella pertussis, Staphylococcus aureus, Clostridium tetani (Tetanus), Cornynebacterium diphtheriae (Diphtheria), Haemophilus influenzae B (Hib), Pseudomonas aeruginosa, Streptococcus agalactiae

(Group B Streptococcus), and E. coli. Examples of specific antigens derived from these pathogens are described above.

7. Antigens suitable for use in Elderly or Immunocompromised Individuals

[191] The compositions of the invention may include one or more antigens suitable for use in elderly or immunocompromised individuals. Such individuals may need to be vaccinated more frequently, with higher doses or with adjuvanted formulations to improve their immune response to the targeted antigens. Antigens which may be targeted for use in Elderly or Immunocompromised individuals include antigens derived from one or more of the following pathogens: Neisseria meningitides, Streptococcus pneumoniae, Streptococcus pyogenes (Group A Streptococcus), Moraxella catarrhalis, Bordetella pertussis, Staphylococcus aureus, Staphylococcus epidermis, Clostridium tetani (Tetanus), Cornynebacterium diphtheriae (Diphtheria), Haemophilus influenzae B (Hib), Pseudomonas aeruginosa, Legionella pneumophila, Streptococcus agalactiae (Group B Streptococcus), Enterococcus faecalis, Helicobacter pylori, Clamydia pneumoniae, Orthomyxovirus (influenza), Pneumovirus (RSV), Paramyxovirus (PIV and Mumps), Morbillivirus (measles), Togavirus (Rubella), Enterovirus (polio), HBV, Coronavirus (SARS), Varicella-zoster virus (VZV), Epstein Barr virus (EBV), Cytomegalovirus (CMV). Examples of specific antigens derived from these pathogens are described above.

8. Antigens suitable for use in Adolescent Vaccines

[192] The compositions of the invention may include one or more antigens suitable for use in adolescent subjects. Adolescents may be in need of a boost of a previously administered pediatric antigen. Pediatric antigens which may be suitable for use in adolescents are described above. In addition, adolescents may be targeted to receive antigens derived from an STD pathogen in order to ensure protective or therapeutic immunity before the

beginning of sexual activity. STD antigens which may be suitable for use in adolescents are described above.

9. Antigen Formulations

[193] In other aspects of the invention, methods of producing microparticles having adsorbed antigens are provided. The methods comprise: (a) providing an emulsion by dispersing a mixture comprising (i) water, (ii) a detergent, (iii) an organic solvent, and (iv) a biodegradable polymer selected from the group consisting of a poly(α-hydroxy acid), a polyhydroxy butyric acid, a polycaprolactone, a polyorthoester, a polyanhydride, and a polycyanoacrylate. The polymer is typically present in the mixture at a concentration of about 1% to about 30% relative to the organic solvent, while the detergent is typically present in the mixture at a weight-to-weight detergent-to-polymer ratio of from about 0.00001:1 to about 0.1:1 (more typically about 0.0001:1 to about 0.1:1, about 0.001:1 to about 0.1:1, or about 0.005:1 to about 0.1:1); (b) removing the organic solvent from the emulsion; and (c) adsorbing an antigen on the surface of the microparticles. In certain embodiments, the biodegradable polymer is present at a concentration of about 3% to about 10% relative to the organic solvent.

[194] Microparticles for use herein will be formed from materials that are sterilizable, non-toxic and biodegradable. Such materials include, without limitation, poly(α-hydroxy acid), polyhydroxybutyric acid, polycaprolactone, polyorthoester, polyanhydride, PACA, and polycyanoacrylate. Preferably, microparticles for use with the present invention are derived from a poly(α-hydroxy acid), in particular, from a poly(lactide) ("PLA") or a copolymer of D,L-lactide and glycolide or glycolic acid, such as a poly(D,L-lactide-co-glycolide) ("PLG" or "PLGA"), or a copolymer of D,L-lactide and caprolactone. The microparticles may be derived from any of various polymeric starting materials which have a variety of molecular weights and, in the case of the copolymers such as PLG, a variety of lactide:glycolide ratios, the selection of which will be largely a matter of

choice, depending in part on the coadministered macromolecule. These parameters are discussed more fully below.

[195] Further antigens may also include an outer membrane vesicle (OMV) preparation.

[196] Additional formulation methods and antigens (especially tumor antigens) are provided in U.S. Patent Serial No. 09/581,772.

10. Antigen References

[197] The following references include antigens useful in conjunction with the compositions of the present invention:

1 WO99/24578
2 WO99/36544.
3 WO99/57280.
4 WO00/22430.
5 Tettelin et al. (2000) Science 287:1809-1815.
6 WO96/29412.
7 Pizza et al. (2000) Science 287:1816-1820.
8 PCT WO 01/52885.
9 Bjune et al. (1991) Lancet 338(8775).
10 Fuskasawa et al. (1999) Vaccine 17:2951-2958.
11 Rosenqist et al. (1998) Dev. Biol. Strand 92:323-333.
12 Constantino et al. (1992) Vaccine 10:691-698.
13 Constantino et al. (1999) Vaccine 17:1251-1263.
14 Watson (2000) Pediatr Infect Dis J 19:331-332.
15 Rubin (20000) Pediatr Clin North Am 47:269-285,v.
16 Jedrzejas (2001) Microbiol Mol Biol Rev 65:187-207.
17 filed on 3rd July 2001 claiming priority from GB-0016363.4;WO 02/02606; PCT IB/01/00166.
18 Kalman et al. (1999) Nature Genetics 21:385-389.
19 Read et al. (2000) Nucleic Acids Res 28:1397-406.
20 Shirai et al. (2000) J. Infect. Dis 181(Suppl 3):S524-S527.
21 WO99/27105.
22 WO00/27994.
23 WO00/37494.
24 WO99/28475.
25 Bell (2000) Pediatr Infect Dis J 19:1187-1188.
26 Iwarson (1995) APMIS 103:321-326.

27 Gerlich et al. (1990) Vaccine 8 Suppl:S63-68 & 79-80.
28 Hsu et al. (1999) Clin Liver Dis 3:901-915.
29 GBStofsson et al. (1996) N. Engl. J. Med. 334-:349-355.
30 Rappuoli et al. (1991) TIBTECH 9:232-238.
31 Vaccines (1988) eds. Plotkin & Mortimer. ISBN 0-7216-1946-0.
32 Del Guidice et al. (1998) Molecular Aspects of Medicine 19:1-70.
33 WO93/018150.
34 WO99/53310.
35 WO98/04702.
36 Ross et al. (2001) Vaccine 19:135-142.
37 Sutter et al. (2000) Pediatr Clin North Am 47:287-308.
38 Zimmerman & Spann (1999) Am Fan Physician 59:113-118, 125-126.
39 Dreensen (1997) Vaccine 15 Suppl"S2-6.
40 MMWR Morb Mortal Wkly rep 1998 Jan 16:47(1):12, 9.
41 McMichael (2000) Vaccine19 Suppl 1:S101-107.
42 Schuchat (1999) Lancer 353(9146):51-6.
43 GB patent applications 0026333.5, 0028727.6 & 0105640.7.
44 Dale (1999) Infect Disclin North Am 13:227-43, viii.
45 Ferretti et al. (2001) PNAS USA 98: 4658-4663.
46 Kuroda et al. (2001) Lancet 357(9264):1225-1240; see also pages 1218-1219.
47 Ramsay et al. (2001) Lancet 357(9251):195-196.
48 Lindberg (1999) Vaccine 17 Suppl 2:S28-36.
49 Buttery & Moxon (2000) J R Coil Physicians Long 34:163-168.
50 Ahmad & Chapnick (1999) Infect Dis Clin North Am 13:113-133, vii.
51 Goldblatt (1998) J. Med. Microbiol. 47:663-567.
52 European patent 0 477 508.
53 U.S. Patent No. 5,306,492.
54 WO98/42721.
55 Conjugate Vaccines (eds. Cruse et al.) ISBN 3805549326, particularly vol. 10:48-114.
56 Hermanson (1996) Bioconjugate Techniques ISBN: 012323368 & 012342335X.
57 EP 0372501.
58 EP 0378881.
59 EP 0427347.
60 WO93/17712.
61 WO98/58668.
62 EP 0471177.
63 WO00/56360.
64 WO00/67161.

[198] The contents of all of the above cited patents, patent applications and journal articles are incorporated by reference as if set forth fully herein.

[199] Where a saccharide or carbohydrate antigen is used, it is preferably conjugated to a carrier protein in order to enhance immunogenicity. See Ramsay *et al.* (2001) Lancet 357(9251):195-196; Lindberg (1999) Vaccine 17 Suppl 2:S28-36; Buttery & Moxon (2000) J R Coll Physicians Lond 34:163-168; Ahmad & Chapnick (1999) Infect Dis Clin North Am 13:113-133, vii; Goldblatt (1998) J. Med. Microbiol. 47:563-567; European patent 0 477 508; US Patent No. 5,306,492; WO98/42721; Conjugate Vaccines (eds. Cruse *et al.*) ISBN 3805549326, particularly vol. 10:48-114; Hermanson (1996) Bioconjugate Techniques ISBN: 0123423368 or 012342335X. Preferred carrier proteins are bacterial toxins or toxoids, such as diphtheria or tetanus toxoids. The CRM197 diphtheria toxoid is particularly preferred.

[200] Other carrier polypeptides include the *N. meningitidis* outer membrane protein (EP-A-0372501), synthetic peptides (EP-A-0378881 and EP-A 0427347), heat shock proteins (WO 93/17712 and WO 94/03208), pertussis proteins (WO 98/58668 and EP A 0471177), protein D from H. influenzae (WO 00/56360), cytokines (WO 91/01146), lymphokines, hormones, growth factors, toxin A or B from C. difficile (WO 00/61761), iron-uptake proteins (WO 01/72337), etc. Where a mixture comprises capsular saccharide from both serigraphs A and C, it may be preferred that the ratio (w/w) of MenA saccharide:MenC saccharide is greater than 1 (*e.g.*, 2:1, 3:1, 4:1, 5:1, 10:1 or higher). Different saccharides can be conjugated to the same or different type of carrier protein. Any suitable conjugation reaction can be used, with any suitable linker where necessary.

[201] Toxic protein antigens may be detoxified where necessary e.g., detoxification of pertussis toxin by chemical and/or genetic means.

VII. Pharmaceutical Compositions

[202] In some embodiments pharmaceutical compositions of the invention comprise a BibA polypeptide (with or without other active agents, as disclosed above). In other embodiments pharmaceutical compositions comprise a nucleic acid molecule encoding

the BibA polypeptide (with or without nucleic acid molecules encoding other active agents, as described above). Nucleic acid vaccines are described, for example, in Robinson & Torres (1997) *Seminars in Immunology* 9:271-283; Donnelly *et al.* (1997) *Ann. Rev Immunol* 15:617-648; Scott-Taylor & Dalgleish (2000) *Expert Opin Investig Drugs* 9:471-480; Apostolopoulos & Plebanski (2000) *Curr Opin Mol Ther* 2:441-447; Ilan (1999) *Curr Opin Mol Ther* 1:116-120; Dubensky *et al.* (2000) *Mol Med* 6:723-732; Robinson & Pertmer (2000) *Adv Virus Res* 55:1-74; Donnelly *et al.* (2000) *Am J Respir Crit Care Med* 162(4 Pt 2):S190-193Davis (1999) *Mt. Sinai J. Med.* 66:84-90. Typically the nucleic acid molecule is a DNA molecule, *e.g.*, in the form of a plasmid. In other embodiments pharmaceutical compositions comprise antibodies which specifically bind to a BibA polypeptide

[203] Immunogenic compositions of the invention are preferably vaccine compositions. The pH of such compositions preferably is between 6 and 8, preferably about 7. The pH can be maintained by the use of a buffer. The composition can be sterile and/or pyrogen-free. The composition can be isotonic with respect to humans. Vaccines according to the invention may be used either prophylactically or therapeutically, but will typically be prophylactic and can be used to treat animals (including companion and laboratory mammals), particularly humans.

A. Pharmaceutically acceptable carriers

[204] Compositions of the invention will typically, in addition to the components mentioned above, comprise one or more "pharmaceutically acceptable carriers." These include any carrier which does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers typically are large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and lipid aggregates (such as oil droplets or liposomes). Such carriers are well known to those of ordinary skill in the art. A composition may also contain a diluent, such as water, saline, glycerol, *etc.* Additionally,

an auxiliary substance, such as a wetting or emulsifying agent, pH buffering substance, and the like, may be present. A thorough discussion of pharmaceutically acceptable components is available in Gennaro (2000) *Remington: The Science and Practice of Pharmacy*. 20th ed., ISBN:0683306472.

B. Immunoregulatory Agents

1. Adjuvants

[205] Vaccines of the invention may be administered in conjunction with other immunoregulatory agents. In particular, compositions will usually include an adjuvant. Adjuvants for use with the invention include, but are not limited to, one or more of the following set forth below:

a. Mineral Containing Compositions

[206] Mineral containing compositions suitable for use as adjuvants in the invention include mineral salts, such as aluminum salts and calcium salts. The invention includes mineral salts such as hydroxides (*e.g.* oxyhydroxides), phosphates (*e.g.* hydroxyphosphates, orthophosphates), sulfates, etc. (*e.g.* see chapters 8 & 9 of Vaccine Design… (1995) eds. Powell & Newman. ISBN: 030644867X. Plenum.), or mixtures of different mineral compounds (*e.g.* a mixture of a phosphate and a hydroxide adjuvant, optionally with an excess of the phosphate), with the compounds taking any suitable form (*e.g.* gel, crystalline, amorphous, etc.), and with adsorption to the salt(s) being preferred. The mineral containing compositions may also be formulated as a particle of metal salt (WO00/23105).

[207] Aluminum salts may be included in vaccines of the invention such that the dose of Al^{3+} is between 0.2 and 1.0 mg per dose.

[208] In one embodiment the aluminum based adjuvant for use in the present invention is alum (aluminum potassium sulfate ($AlK(SO_4)_2$)), or an alum derivative, such as that formed in-

situ by mixing an antigen in phosphate buffer with alum, followed by titration and precipitation with a base such as ammonium hydroxide or sodium hydroxide.

[209] Another aluminum-based adjuvant for use in vaccine formulations of the present invention is aluminum hydroxide adjuvant ($Al(OH)_3$) or crystalline aluminum oxyhydroxide (AlOOH), which is an excellent adsorbant, having a surface area of approximately $500m^2/g$. Alternatively, aluminum phosphate adjuvant ($AlPO_4$) or aluminum hydroxyphosphate, which contains phosphate groups in place of some or all of the hydroxyl groups of aluminum hydroxide adjuvant is provided. Preferred aluminum phosphate adjuvants provided herein are amorphous and soluble in acidic, basic and neutral media.

[210] In another embodiment the adjuvant of the invention comprises both aluminum phosphate and aluminum hydroxide. In a more particular embodiment thereof, the adjuvant has a greater amount of aluminum phosphate than aluminum hydroxide, such as a ratio of 2:1, 3:1, 4:1, 5:1, 6:1, 7:1, 8:1, 9:1 or greater than 9:1, by weight aluminum phosphate to aluminum hydroxide. More particular still, aluminum salts in the vaccine are present at 0.4 to 1.0 mg per vaccine dose, or 0.4 to 0.8 mg per vaccine dose, or 0.5 to 0.7 mg per vaccine dose, or about 0.6 mg per vaccine dose.

[211] Generally, the preferred aluminum-based adjuvant(s), or ratio of multiple aluminum-based adjuvants, such as aluminum phosphate to aluminum hydroxide is selected by optimization of electrostatic attraction between molecules such that the antigen carries an opposite charge as the adjuvant at the desired pH. For example, aluminum phosphate adjuvant (isoelectric point = 4) adsorbs lysozyme, but not albumin at pH 7.4. Should albumin be the target, aluminum hydroxide adjuvant would be selected (iep 11.4). Alternatively, pretreatment of aluminum hydroxide with phosphate lowers its isoelectric point, making it a preferred adjuvant for more basic antigens.

b. Oil-Emulsions

[212] Oil-emulsion compositions suitable for use as adjuvants in the invention include squalene-water emulsions, such as MF59 (5% Squalene, 0.5% TWEEN™ 80, and 0.5% Span 85, formulated into submicron particles using a microfluidizer). See WO90/14837. See also, Podda, Vaccine (2001) 19: 2673-2680; Frey *et al.*, Vaccine (2003) 21:4234-4237. MF59 is used as the adjuvant in the FLUAD™ influenza virus trivalent subunit vaccine.

[213] Particularly preferred adjuvants for use in the compositions are submicron oil-in-water emulsions. Preferred submicron oil-in-water emulsions for use herein are squalene/water emulsions optionally containing varying amounts of MTP-PE, such as a submicron oil-in-water emulsion containing 4-5% w/v squalene, 0.25-1.0% w/v TWEEN™ 80□ (polyoxyelthylenesorbitan monooleate), and/or 0.25-1.0% SPAN 85™ (sorbitan trioleate), and, optionally, N-acetylmuramyl-L-alanyl-D-isogluatminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-huydroxyphosphophoryloxy)-ethylamine (MTP-PE), for example, the submicron oil-in-water emulsion known as "MF59" (International Publication No. WO90/14837; US Patent Nos. 6,299,884 and 6,451,325, and Ott *et al.*, in Vaccine Design: The Subunit and Adjuvant Approach (Powell, M.F. and Newman, M.J. eds.) Plenum Press, New York, 1995, pp. 277-296). MF59 contains 4-5% w/v Squalene (*e.g.* 4.3%), 0.25-0.5% w/v TWEEN™ 80, and 0.5% w/v SPAN 85™ and optionally contains various amounts of MTP-PE, formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, MA). For example, MTP-PE may be present in an amount of about 0-500 μg/dose, more preferably 0-250 μg/dose and most preferably, 0-100 μg/dose. As used herein, the term "MF59-0" refers to the above submicron oil-in-water emulsion lacking MTP-PE, while the term MF59-MTP denotes a formulation that contains MTP-PE. For instance, "MF59-100" contains 100 μg MTP-PE per dose, and so on. MF69, another submicron oil-in-water emulsion for use herein, contains 4.3% w/v squalene, 0.25% w/v TWEEN™ 80, and 0.75% w/v SPAN 85™ and optionally MTP-PE. Yet another submicron oil-in-water

emulsion is MF75, also known as SAF, containing 10% squalene, 0.4% TWEEN™ 80, 5% pluronic-blocked polymer L121, and thr-MDP, also microfluidized into a submicron emulsion. MF75-MTP denotes an MF75 formulation that includes MTP, such as from 100-400 μg MTP-PE per dose.

[214] Submicron oil-in-water emulsions, methods of making the same and immunostimulating agents, such as muramyl peptides, for use in the compositions, are described in detail in WO90/14837 and U.S. Patents 6,299,884 and 6,45 1,325.

[215] Complete Freund's adjuvant (CFA) and incomplete Freund's adjuvant (IFA) may also be used as adjuvants in the invention.

c. Saponin Formulations

[216] Saponin formulations, may also be used as adjuvants in the invention. Saponins are a heterologous group of sterol glycosides and triterpenoid glycosides that are found in the bark, leaves, stems, roots and even flowers of a wide range of plant species. Saponins isolated from the bark of the Quillaia saponaria Molina tree have been widely studied as adjuvants. Saponins can also be commercially obtained from Smilax ornata (sarsaprilla), Gypsophilla paniculata (brides veil), and Saponaria officianalis (soap root). Saponin adjuvant formulations include purified formulations, such as QS21, as well as lipid formulations, such as ISCOMs.

[217] Saponin compositions have been purified using High Performance Thin Layer Chromatography (HP-TLC) and Reversed Phase High Performance Liquid Chromatography (RP-HPLC). Specific purified fractions using these techniques have been identified, including QS7, QS17, QS18, QS21, QH-A, QH-B and QH-C. Preferably, the saponin is QS21. A method of production of QS21 is disclosed in U.S. Patent 5,057,540. Saponin formulations may also comprise a sterol, such as cholesterol (see WO96/33739).

[218] Combinations of saponins and cholesterols can be used to form unique particles called Immunostimulating Complexes (ISCOMs). ISCOMs typically also include a phospholipid such as phosphatidylethanolamine or phosphatidylcholine. Any known saponin can be used in ISCOMs. Preferably, the ISCOM includes one or more of Quil A, QHA and QHC. ISCOMs are further described in EP0109942, WO96/11711 and WO96/33739. Optionally, the ISCOMS may be devoid of (an) additional detergent(s). See WO00/07621.

[219] A review of the development of saponin based adjuvants can be found in Barr, *et al.*, Advanced Drug Delivery Reviews (1998) 32:247-271. *See also* Sjolander, *et al.*, Advanced Drug Delivery Reviews (1998) 32:321-338.

d. Virosomes and Virus Like Particles (VLPs)

[220] Virosomes and Virus Like Particles (VLPs) can also be used as adjuvants in the invention. These structures generally contain one or more proteins from a virus optionally combined or formulated with a phospholipid. They are generally non-pathogenic, non-replicating and generally do not contain any of the native viral genome. The viral proteins may be recombinantly produced or isolated from whole viruses. These viral proteins suitable for use in virosomes or VLPs include proteins derived from influenza virus (such as HA or NA), Hepatitis B virus (such as core or capsid proteins), Hepatitis E virus, measles virus, Sindbis virus, Rotavirus, Foot-and-Mouth Disease virus, Retrovirus, Norwalk virus, human Papilloma virus, HIV, RNA-phages, Qß-phage (such as coat proteins), GA-phage, fr-phage, AP205 phage, and Ty (such as retrotransposon Ty protein p1). VLPs are discussed further in WO03/024480, WO03/024481, and Niikura *et al.*, Virology (2002) 293:273-280; Lenz *et al.*, Journal of Immunology (2001) 5246-5355; Pinto, *et al.*, Journal of Infectious Diseases (2003) 188:327-338; and Gerber *et al.*, Journal of Virology (2001) 75(10):4752-4760. Virosomes are discussed further in, for example, Gluck *et al.*, Vaccine (2002) 20:B10 –B16. Immunopotentiating reconstituted influenza virosomes (IRIV) are used as the subunit antigen delivery system in the

intranasal trivalent INFLEXAL™ product {Mischler & Metcalfe (2002) Vaccine 20 Suppl 5:B17-23} and the INFLUVAC PLUS™ product.

e. Bacterial or Microbial Derivatives

[221] Adjuvants suitable for use in the invention include bacterial or microbial derivatives such as:

i. Non-toxic derivatives of enterobacterial lipopolysaccharide (LPS)

[222] Such derivatives include Monophosphoryl lipid A (MPL) and 3-O-deacylated MPL (3dMPL). 3dMPL is a mixture of 3 De-O-acylated monophosphoryl lipid A with 4, 5 or 6 acylated chains. A preferred "small particle" form of 3 De-O-acylated monophosphoryl lipid A is disclosed in EP 0 689 454. Such "small particles" of 3dMPL are small enough to be sterile filtered through a 0.22 micron membrane (see EP 0 689 454). Other non-toxic LPS derivatives include monophosphoryl lipid A mimics, such as aminoalkyl glucosaminide phosphate derivatives *e.g.* RC 529. See Johnson *et al.* (1999) Bioorg Med Chem Lett 9:2273-2278.

ii. Lipid A Derivatives

[223] Lipid A derivatives include derivatives of lipid A from Escherichia coli such as OM-174. OM-174 is described for example in Meraldi *et al.*, Vaccine (2003) 21:2485-2491; and Pajak, *et al.*, Vaccine (2003) 21:836-842.

f. Immunostimulatory oligonucleotides

[224] Immunostimulatory oligonucleotides suitable for use as adjuvants in the invention include nucleotide sequences containing a CpG motif (a sequence containing an unmethylated cytosine followed by guanosine and linked by a phosphate bond). Bacterial double stranded RNA or oligonucleotides containing palindromic or poly(dG) sequences have also been shown to be immunostimulatory.

[225] The CpG's can include nucleotide modifications/analogs such as phosphorothioate modifications and can be double-stranded or single-stranded. Optionally, the guanosine may be replaced with an analog such as 2'-deoxy-7-deazaguanosine. See Kandimalla, *et al.*, Nucleic Acids Research (2003) 31(9): 2393-2400; WO02/26757 and WO99/62923 for examples of possible analog substitutions. The adjuvant effect of CpG oligonucleotides is further discussed in Krieg, Nature Medicine (2003) 9(7): 831-835; McCluskie, *et al.*, FEMS Immunology and Medical Microbiology (2002) 32:179-185; WO98/40100; US Patent No. 6,207,646; US Patent No. 6,239,116 and US Patent No. 6,429,199.

[226] The CpG sequence may be directed to TLR9, such as the motif GTCGTT or TTCGTT. See Kandimalla, *et al.*, Biochemical Society Transactions (2003) 31 (part 3): 654-658. The CpG sequence may be specific for inducing a Th1 immune response, such as a CpG-A ODN, or it may be more specific for inducing a B cell response, such a CpG-B ODN. CpG-A and CpG-B ODNs are discussed in Blackwell, *et al.*, J. Immunol. (2003) 170(8):4061-4068; Krieg, TRENDS in Immunology (2002) 23(2): 64-65 and WO01/95935. Preferably, the CpG is a CpG-A ODN.

[227] Preferably, the CpG oligonucleotide is constructed so that the 5' end is accessible for receptor recognition. Optionally, two CpG oligonucleotide sequences may be attached at their 3' ends to form "immunomers". See, for example, Kandimalla, *et al.*, BBRC (2003) 306:948-953; Kandimalla, *et al.*, Biochemical Society Transactions (2003) 31(part 3):664-658; Bhagat *et al.*, BBRC (2003) 300:853-861 and WO03/035836.

g. ADP-ribosylating toxins and detoxified derivatives thereof

[228] Bacterial ADP-ribosylating toxins and detoxified derivatives thereof may be used as adjuvants in the invention. Preferably, the protein is derived from *E. coli* (*i.e.*, *E. coli* heat labile enterotoxin "LT), cholera ("CT"), or pertussis ("PT"). The use of detoxified ADP-ribosylating toxins as mucosal adjuvants is described in WO95/17211 and as parenteral adjuvants in WO98/42375. Preferably, the adjuvant is a detoxified LT mutant such as

LT-K63, LT-R72, and LTR192G. The use of ADP-ribosylating toxins and detoxified derivatives thereof, particularly LT-K63 and LT-R72, as adjuvants can be found in the following references: Beignon, *et al.*, Infection and Immunity (2002) 70(6):3012-3019; Pizza, *et al.*, Vaccine (2001) 19:2534-2541; Pizza, *et al.*, Int. J. Med. Microbiol (2000) 290(4-5):455-461; Scharton-Kersten *et al.*, Infection and Immunity (2000) 68(9):5306-5313; Ryan *et al.*, Infection and Immunity (1999) 67(12):6270-6280; Partidos *et al.*, Immunol. Lett. (1999) 67(3):209-216; Peppoloni *et al.*, Vaccines (2003) 2(2):285-293; and Pine *et al.*, (2002) J. Control Release (2002) 85(1-3):263-270. Numerical reference for amino acid substitutions is preferably based on the alignments of the A and B subunits of ADP-ribosylating toxins set forth in Domenighini *et al.*, Mol. Microbiol (1995) 15(6):1165-1167.

h. Bioadhesives and Mucoadhesives

[229] Bioadhesives and mucoadhesives may also be used as adjuvants in the invention. Suitable bioadhesives include esterified hyaluronic acid microspheres (Singh *et al.* (2001) J. Cont. Rele. 70:267-276) or mucoadhesives such as cross-linked derivatives of polyacrylic acid, polyvinyl alcohol, polyvinyl pyrollidone, polysaccharides and carboxymethylcellulose. Chitosan and derivatives thereof may also be used as adjuvants in the invention. *See* WO99/27960.

i. Microparticles

[230] Microparticles may also be used as adjuvants in the invention. Microparticles (*i.e.* a particle of ~100nm to ~150μm in diameter, more preferably ~200nm to ~30μm in diameter, and most preferably ~500nm to ~10μm in diameter) formed from materials that are biodegradable and non toxic (*e.g.* a poly(α-hydroxy acid), a polyhydroxybutyric acid, a polyorthoester, a polyanhydride, a polycaprolactone, etc.), with poly(lactide co glycolide) are preferred, optionally treated to have a negatively-charged surface (*e.g.* with SDS) or a positively-charged surface (*e.g.* with a cationic detergent, such as CTAB).

j. Liposomes

[231] Examples of liposome formulations suitable for use as adjuvants are described in US Patent No. 6,090,406, US Patent No. 5,916,588, and EP 0 626 169.

k. Polyoxyethylene ether and Polyoxyethylene Ester Formulations

[232] Adjuvants suitable for use in the invention include polyoxyethylene ethers and polyoxyethylene esters. WO99/52549. Such formulations further include polyoxyethylene sorbitan ester surfactants in combination with an octoxynol (WO01/21207) as well as polyoxyethylene alkyl ethers or ester surfactants in combination with at least one additional non-ionic surfactant such as an octoxynol (WO01/21152).

[233] Preferred polyoxyethylene ethers are selected from the following group: polyoxyethylene-9-lauryl ether (laureth 9), polyoxyethylene-9-steoryl ether, polyoxytheylene-8-steoryl ether, polyoxyethylene-4-lauryl ether, polyoxyethylene-35-lauryl ether, and polyoxyethylene-23-lauryl ether.

l. Polyphosphazene (PCPP)

[234] PCPP formulations are described, for example, in Andrianov *et al.*, "Preparation of hydrogel microspheres by coacervation of aqueous polyphophazene solutions", Biomaterials (1998) 19(1-3):109-115 and Payne *et al.*, "Protein Release from Polyphosphazene Matrices", Adv. Drug. Delivery Review (1998) 31(3):185-196.

m. Muramyl peptides

[235] Examples of muramyl peptides suitable for use as adjuvants in the invention include N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-l-alanyl-d-isoglutamine (nor-MDP), and N acetylmuramyl-l-alanyl-d-isoglutaminyl-l-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine MTP-PE).

n. Imidazoquinoline Compounds

[236] Examples of imidazoquinoline compounds suitable for use adjuvants in the invention include Imiquimod and its analogues, described further in Stanley, Clin Exp Dermatol (2002) 27(7):571-577; Jones, Curr Opin Investig Drugs (2003) 4(2):214-218; and U.S. Patents 4,689,338, 5,389,640, 5,268,376, 4,929,624, 5,266,575, 5,352,784, 5,494,916, 5,482,936, 5,346,905, 5,395,937, 5,238,944, and 5,525,612.

o. Thiosemicarbazone Compounds

[237] Examples of thiosemicarbazone compounds, as well as methods of formulating, manufacturing, and screening for compounds all suitable for use as adjuvants in the invention include those described in WO04/60308. The thiosemicarbazones are particularly effective in the stimulation of human peripheral blood mononuclear cells for the production of cytokines, such as TNF- α.

p. Tryptanthrin Compounds

[238] Examples of tryptanthrin compounds, as well as methods of formulating, manufacturing, and screening for compounds all suitable for use as adjuvants in the invention include those described in WO04/64759. The tryptanthrin compounds are particularly effective in the stimulation of human peripheral blood mononuclear cells for the production of cytokines, such as TNF- α.

[239] The invention may also comprise combinations of aspects of one or more of the adjuvants identified above. For example, the following adjuvant compositions may be used in the invention:

(1) a saponin and an oil-in-water emulsion (WO99/11241);

(2) a saponin (*e.g.*, QS21) + a non-toxic LPS derivative (*e.g.* 3dMPL) (see WO94/00153);

(3) a saponin (*e.g.*, QS21) + a non-toxic LPS derivative (*e.g.* 3dMPL) + a cholesterol;

(4) a saponin (*e.g.*, QS21) + 3dMPL + IL 12 (optionally + a sterol) (WO98/57659);

(5) combinations of 3dMPL with, for example, QS21 and/or oil-in-water emulsions (See European patent applications 0835318, 0735898 and 0761231);

(6) SAF, containing 10% Squalane, 0.4% Tween 80, 5% pluronic-block polymer L121, and thr-MDP, either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion.

(7) RibiTM adjuvant system (RAS), (Ribi Immunochem) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (Detox™); and

(8) one or more mineral salts (such as an aluminum salt) + a non-toxic derivative of LPS (such as 3dPML).

(9) one or more mineral salts (such as an aluminum salt) + an immunostimulatory oligonucleotide (such as a nucleotide sequence including a CpG motif).

q. Human Immunomodulators

[240] Human immunomodulators suitable for use as adjuvants in the invention include cytokines, such as interleukins (*e.g.* IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, etc.), interferons (*e.g.* interferon-γ), macrophage colony stimulating factor, and tumor necrosis factor.

[241] Aluminum salts and MF59 are preferred adjuvants for use with injectable influenza vaccines. Bacterial toxins and bioadhesives are preferred adjuvants for use with mucosally-delivered vaccines, such as nasal vaccines.

[242] The contents of all of the above cited patents, patent applications and journal articles are incorporated by reference as if set forth fully herein.

VIII. Therapeutic methods

[243] The invention provides methods for inducing or increasing an immune response to *S. agalactiae* using the compositions described above. The immune response is preferably protective and can include antibodies and/or cell-mediated immunity (including systemic and mucosal immunity). Immune responses include booster responses. Compositions comprising antibodies can be used to treat *S. agalactiae* infections.

[244] Diseases caused by GBS which can be prevented or treated according to the invention include, but are not limited to, sepsis, meningitis in newborns, and newborn pneumonia. The compositions may also be effective against other streptococcal bacteria, *e.g.*, GBS.

A. Tests to determine the efficacy of the immune response

[245] One way of assessing efficacy of therapeutic treatment involves monitoring GBS infection after administration of the composition of the invention. One way of assessing efficacy of prophylactic treatment involves monitoring immune responses against the GBS antigens in the compositions of the invention after administration of the composition.

[246] Another way of assessing the immunogenicity of the component proteins of the immunogenic compositions of the present invention is to express the proteins recombinantly and to screen patient sera or mucosal secretions by immunoblot. A positive reaction between the protein and the patient serum indicates that the patient has previously mounted an immune response to the protein in question; i.e., the protein is an

immunogen. This method may also be used to identify immunodominant proteins and/or epitopes.

[247] Another way of checking efficacy of therapeutic treatment involves monitoring GBS infection after administration of the compositions of the invention. One way of checking efficacy of prophylactic treatment involves monitoring immune responses both systemically (such as monitoring the level of IgG1 and IgG2a production) and mucosally (such as monitoring the level of IgA production) against the GBS antigens in the compositions of the invention after administration of the composition. Typically, GBS serum specific antibody responses are determined post-immunization but pre-challenge whereas mucosal GBS-specific antibody body responses are determined post-immunization and post-challenge.

[248] The vaccine compositions of the present invention can be evaluated in *in vitro* and *in vivo* animal models prior to host, *e.g.*, human, administration. A particularly useful mouse model is the Active Maternal Immunization assay described in Example 21, below. This is an *in vivo* protection assay in which female mice are immunized with the test antigen composition. The female mice are then bred and their pups are challenged with a lethal dose of GBS. Serum titers of the female mice during the immunization schedule are measured as well as the survival time of the pups after challenge.

[249] For example, groups of 4 CD-1 outbred female mice 6-8 weeks old (Charles River Laboratories, Calco Italy) are immunized with one or more GBS antigens (*e.g.*, 20 μg of a BibA polypeptide suspended in 100 μl of PBS). Each group receives 3 doses at days 0, 21 and 35. Immunization is performed through intra-peritoneal injection of the protein with an equal volume of Complete Freund's Adjuvant (CFA) for the first dose and Incomplete Freund's Adjuvant (IFA) for the following two doses. In each immunization scheme negative and positive control groups are used. Immune response is monitored by using serum samples taken on day 0 and 49. The sera are analyzed as pools from each group of mice.

[250] The immune response may be one or both of a TH1 immune response and a TH2 response. The immune response may be an improved or an enhanced or an altered immune response. The immune response may be one or both of a systemic and a mucosal immune response. Preferably the immune response is an enhanced system and/or mucosal response.

[251] An enhanced systemic and/or mucosal immunity is reflected in an enhanced TH1 and/or TH2 immune response. Preferably, the enhanced immune response includes an increase in the production of IgG1 and/or IgG2a and/or IgA.

[252] Preferably the mucosal immune response is a TH2 immune response. Preferably, the mucosal immune response includes an increase in the production of IgA.

[253] Activated TH2 cells enhance antibody production and are therefore of value in responding to extracellular infections. Activated TH2 cells may secrete one or more of IL-4, IL-5, IL-6, and IL-10. A TH2 immune response may result in the production of IgG1, IgE, IgA and memory B cells for future protection.

[254] A TH2 immune response may include one or more of an increase in one or more of the cytokines associated with a TH2 immune response (such as IL-4, IL-5, IL-6 and IL-10), or an increase in the production of IgG1, IgE, IgA and memory B cells. Preferably, the enhanced TH2 immune response will include an increase in IgG1 production.

[255] A TH1 immune response may include one or more of an increase in CTLs, an increase in one or more of the cytokines associated with a TH1 immune response (such as IL-2, IFNγ, and TNFβ), an increase in activated macrophages, an increase in NK activity, or an increase in the production of IgG2a. Preferably, the enhanced TH1 immune response will include an increase in IgG2a production.

[256] Immunogenic compositions of the invention, in particular, immunogenic composition comprising a BibA polypeptide of the present invention (or nucleic acid molecule encoding a BibA polypeptide) may be used either alone or in combination with other

GBS antigens optionally with an immunoregulatory agent capable of eliciting a Th1 and/or Th2 response.

[257] The invention also comprises an immunogenic composition comprising one or more immunoregulatory agent, such as a mineral salt, such as an aluminium salt and an oligonucleotide containing a CpG motif. Most preferably, the immunogenic composition includes both an aluminium salt and an oligonucleotide containing a CpG motif. Alternatively, the immunogenic composition includes an ADP ribosylating toxin, such as a detoxified ADP ribosylating toxin and an oligonucleotide containing a CpG motif. Preferably, one or more of the immunoregulatory agents include an adjuvant. The adjuvant may be selected from one or more of the group consisting of a TH1 adjuvant and TH2 adjuvant, further discussed below.

[258] The compositions of the invention will preferably elicit both a cell mediated immune response as well as a humoral immune response in order to effectively address a GBS infection. This immune response will preferably induce long lasting (*e.g.*, neutralizing) antibodies and a cell mediated immunity that can quickly respond upon exposure to a BibA polypeptide.

[259] In addition to a BibA polypeptide (or nucleic acid molecule encoding a BibA polypeptide), an immunogenic composition can comprise one or more GBS antigen(s) which elicits a neutralizing antibody response and one or more GBS antigen(s) which elicit a cell mediated immune response. In this way, the neutralizing antibody response prevents or inhibits an initial GBS infection while the cell-mediated immune response capable of eliciting an enhanced Th1 cellular response prevents further spreading of the GBS infection. Preferably, the immunogenic composition comprises one or more GBS surface antigens and one or more GBS cytoplasmic antigens, such as a cytoplasmic antigen capable of eliciting a Th1 cellular response.

B. Preparation of Compositions

[260] The compositions of the invention may be prepared in various forms. For example, a composition can be prepared as an injectable, either as a liquid solution or a suspension. Solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared (*e.g.*, a lyophilized composition). A composition can be prepared for oral administration, such as a tablet or capsule, as a spray, or as a syrup (optionally flavored). A composition can be prepared for pulmonary administration, *e.g.*, as an inhaler, using a fine powder or a spray. A composition can be prepared as a suppository or pessary. A composition can be prepared for nasal, aural or ocular administration *e.g.*, as drops. A composition can be in kit form, designed such that a combined composition is reconstituted just prior to administration to a patient. Such kits may comprise one or more GBS or other antigens in liquid form and one or more lyophilized antigens.

[261] Immunogenic compositions used as vaccines comprise an immunologically effective amount of a BibA polypeptide (or a nucleic acid molecule encoding a BibA polypeptide) or BibA antibodies, as well as any other components, as needed, such as antibiotics. An "immunologically effective amount" is an amount which, when administered to an individual, either in a single dose or as part of a series, increases a measurable immune response or prevents or reduces a clinical symptom.

[262] In another embodiment, the antibiotic is administered subsequent to the administration of a composition of the invention or the composition comprising the one or more surface-exposed and/or surface-associated GBS antigens of the invention. Examples of antibiotics suitable for use in the treatment of a GBS infection include but are not limited to penicillin or a derivative thereof.

C. Methods of Administration

[263] Compositions of the invention will generally be administered directly to a patient. The compositions of the present invention may be administered, either alone or as part of a composition, via a variety of different routes. Certain routes may be favored for certain compositions, as resulting in the generation of a more effective immune response,

preferably a CMI response, or as being less likely to induce side effects, or as being easier for administration.

[264] Delivery methods include parenteral injection (*e.g.*, subcutaneous, intraperitoneal, intravenous, intramuscular, or interstitial injection) and rectal, oral (*e.g.*, tablet, spray), vaginal, topical, transdermal (*e.g.*, see WO 99/27961), transcutaneous (*e.g.*, see WO02/074244 and WO02/064162), intranasal (*e.g.*, see WO03/028760), ocular, aural, and pulmonary or other mucosal administration.

[265] By way of example, the compositions of the present invention may be administered via a systemic route or a mucosal route or a transdermal route or it may be administered directly into a specific tissue. As used herein, the term "systemic administration" includes but is not limited to any parenteral routes of administration. In particular, parenteral administration includes but is not limited to subcutaneous, intraperitoneal, intravenous, intraarterial, intramuscular, or intrasternal injection, intravenous, intraarterial, or kidney dialytic infusion techniques. Preferably, the systemic, parenteral administration is intramuscular injection. As used herein, the term "mucosal administration" includes but is not limited to oral, intranasal, intravaginal, intrarectal, intratracheal, intestinal and ophthalmic administration.

[266] Teenagers and children, including toddlers and infants, can receive a vaccine for prophylactic use; therapeutic vaccines typically are administered to teenagers or adults. A vaccine intended for children may also be administered to adults *e.g.,* to assess safety, dosage, immunogenicity, *etc.*

[267] The immunogenic compositions of the present invention may be administered in combination with an antibiotic treatment regime. In one embodiment, the antibiotic is administered prior to administration of a composition of the invention.

[268] Dosage treatment can be a single dose schedule or a multiple dose schedule. Multiple doses may be used in a primary immunization schedule and/or in a booster immunization

schedule. In a multiple dose schedule the various doses may be given by the same or different routes *e.g.*, a parenteral prime and mucosal boost, a mucosal prime and parenteral boost, etc.

[269] The amount of active agent in a composition varies depending upon the health and physical condition of the individual to be treated, age, the taxonomic group of individual to be treated (*e.g.*, non-human primate, primate, *etc.*), the capacity of the individual's immune system to synthesize antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors. The amount will fall in a relatively broad range which can be determined through routine trials.

IX. Kits

[270] The invention also provides kits comprising one or more containers of compositions of the invention or their components. Compositions can be in liquid form or can be lyophilized, as can individual components of the compositions. Suitable containers for the compositions include, for example, bottles, vials, syringes, and test tubes. Containers can be formed from a variety of materials, including glass or plastic. A container may have a sterile access port (for example, the container may be an intravenous solution bag or a vial having a stopper pierceable by a hypodermic injection needle).

[271] The kit can further comprise a second container comprising a pharmaceutically-acceptable buffer, such as phosphate-buffered saline, Ringer's solution, or dextrose solution. It can also contain other materials useful to the end-user, including other buffers, diluents, filters, needles, and syringes. The kit can also comprise a second or third container with another active agent, for example an antibiotic.

[272] The kit can also comprise a package insert containing written instructions for methods of inducing immunity against *S. agalactiae*. The package insert can be an unapproved draft

package insert or can be a package insert approved by the Food and Drug Administration (FDA) or other regulatory body.

X. Screening methods

[273] The invention provides assays for screening test compounds that bind to or modulate the activity of BibA. A test compound preferably (1) binds to the coiled-coil domain and blocks the interaction of BibA with complement, *e.g.*, C4 binding protein, or the formation of BibA dimers; or (b) binds to the proline-rich domain and blocks the binding of BibA to host epithelial cells; (c) binds to the N-terminal domain of BibA and blocks the binding of BibA to IgA; or (d) binds to various portions of BibA and blocks the binding of IgG to the protein. Assays can be carried out using full-length BibA protein or BibA polypeptides of the invention.

A. Test compounds

[274] Test compounds can be pharmacologic agents already known in the art or can be compounds previously unknown to have any pharmacological activity. The compounds can be naturally occurring or designed in the laboratory. They can be isolated from microorganisms, animals, or plants, can be produced recombinantly, synthesized by chemical methods known in the art, or obtained using any of the numerous combinatorial library methods known in the art, including but not limited to, biological libraries, spatially addressable parallel solid phase or solution phase libraries, synthetic library methods requiring deconvolution, the "one-bead one-compound" library method, and synthetic library methods using affinity chromatography selection.

B. Assays

[275] Any method known in the art can be used to detect binding between a test compound and a domain of BibA or disruption of binding between a domain of BibA and its biological target.

[276] In some binding assays, either the test compound or the BibA protein or polypeptide can comprise a detectable label, such as a fluorescent, radioisotopic, chemiluminescent, or enzymatic label, such as horseradish peroxidase, alkaline phosphatase, or luciferase. Methods of detecting such labels are well known in the art. Alternatively, binding can be determined without labeling either of the interactants. *See, e.g.*, McConnell *et al.*, *Science 257*, 1906-12, 1992. Technologies such as real-time Bimolecular Interaction Analysis (BIA) (Sjolander & Urbaniczky, *Anal. Chem. 63*, 2338-2345, 1991, and Szabo *et al.*, *Curr. Opin. Struct. Biol. 5*, 699-705, 1995) also can be used.

[277] In other embodiments, a BibA protein or polypeptide can be used as a "bait protein" in a two-hybrid assay or three-hybrid assay (see, *e.g.*, U.S. Patent 5,283,317; Zervos *et al.*, *Cell 72*, 223-232, 1993; Madura *et al.*, *J. Biol. Chem. 268*, 12046-12054, 1993; Bartel *et al.*, *BioTechniques 14*, 920-924, 1993; Iwabuchi *et al.*, *Oncogene 8*, 1693-1696, 1993; and Brent W094/10300), to identify other proteins which bind to or interact with various domains of BibA.

[278] Assays such as those described in the Examples below can be used to detect whether binding between various domains of BibA and the biological targets of those domains is disrupted or prevented by a test compound.

[279] All patents, patent applications, and references cited in this disclosure are expressly incorporated herein by reference in their entireties. The above disclosure generally describes the present invention. A more complete understanding can be obtained by reference to the following specific examples, which are provided for purposes of illustration only and are not intended to limit the scope of the invention.

EXAMPLE 1

BibA can form dimers

[280] This example demonstrates that BibA can form dimers. In a high-resolution fractionation, molecules elute from the matrix pores in order of decreasing size. Smaller molecules have greater access to the pores of the matrix and hence move down the column. See **FIGS. 3A** and **3B**.

EXAMPLE 2

BibA protein surface-association

[281] GBS bacteria were incubated with secondary FITC-conjugated α-mouse IgG antibody alone. Bacteria were also treated with mouse serum immunized with Freund adjuvant (α-PBS) as a negative control. **FIGS. 4A** and **4B** illustrate the negative control on plots labeled "α-PBS." BibA levels are expressed as a change in mean of fluorescence between cells treated with α-BibA serum and pre-immune serum. Bacteria incubated with pre-immune serum were compared to bacteria treated with α-BibA serum to obtain a change in mean of fluorescence (Δ mean).

[282] BibA protein of strains 2603, 18RS21 and H36B exhibited surface-association but strains 515 and CJB111 did not (Δmean = 0). See also **FIG. 5**.

EXAMPLE 3

BibA protein clusters

[283] GBS strain 515 (pAM401-SAG2063) was grown overnight in THB medium (10 ml). Bacterial cells from 1 ml of the overnight culture were resuspended in 5 ml of fresh THB medium and grown at 37°C up to OD 0.5 (stationary phase). Bacteria were then centrifuged for 10 minutes at 3000 rpm at room temperature, washed, and resuspended in

1 ml of PBS. Formvar-carbon-coated nickel grids were floated on drops of GBS suspensions for 10 minutes. The grids were then fixed in 2% PFA for 15 minutes and placed in blocking solution (PBS containing 1% normal rabbit serum and 1% BSA). The grids were then floated on drops of primary antiserum against BibA (mαBibA) diluted 1:50 in blocking solution for 30 minutes at room temperature, washed with 6 drops of blocking solution, and floated on secondary antibody conjugated to 10 nm gold particles diluted 1:25 in 1% BSA for 30 minutes. The grids were then washed with 4 drops of PBS and then with 4 drops of distilled water and air dried. The grids were examined using a GEOL 1200 EX 11 transmission electron microscope.

[284] **FIG. 6** shows the presence of BibA protein clusters.

EXAMPLE 4

BibA expression on the surface of strain 515 pAM401

[285] BibA gene (SAG2063) including its own promoter and terminator was cloned into pAM401 vector using BamH1 and SalI restriction sites as illustrated in **FIG. 7A**. GBS strains 2603 V/R and 515 Ia were transformed with this construct.

[286] FACS analysis showed that BibA protein is exposed on the 515 (pAM401-SAG2063) surface at high levels. **FIG. 7B**.

EXAMPLE 5

Increased expression of BibA on the surface of strain 2603

[287] FACS analysis showed that the exposure of BibA protein on the 2603 (pAM401-SAG2063) surface is increased respect the 2603 wt strain. The results are shown in **FIG. 8**.

EXAMPLE 6

Secreted form of BibA

[288] GBS protein extracts were separated via SDS-PAGE and transferred to a nitrocellulose membrane. Proteins were then overlaid with a mouse α-BibA polyclonal antibody and stained with HRP-conjugated secondary antibody. As **FIG. 10** illustrates, in the separation of BibA strains 515 and CJB111, the BibA protein was found only in the culture supernatant (the secreted protein fraction). This demonstrates that the truncated form of the BibA protein in strains 515 and CJB111, which lack the proline-rich motif, is expressed in the secreted. **See FIG. 10.**

EXAMPLE 7

BibA binds C4 binding protein (C4BP)

[289] Recombinant BibA proteins were dried onto a nitrocellulose membrane and incubated with recombinant c4-binding protein. Bound protein was then detected using a mouse a-C4BP monoclonal antibody and stained with HRP-conjugated antibody. **FIG. 11A** is a dot blot in which BibA protein at different concentrations is stained with the HRP-conjugated antibody, demonstrating that BibA binds C4 binding protein.

[290] Recombinant BibA protein was separated by SDS-PAGE, blotted onto a nitrocellulose membrane and then incubated with recombinant C4-binding protein. Bound protein was then detected using a mouse a-C4BP monoclonal antibody and stained with HRP-conjugated antibody. **FIG. 11B** shows a Western blot that confirms that BibA binds C4 binding protein.

EXAMPLE 8

BibA protein binds to the surface of epithelial cells

[291] ME180 cervical cells were incubated both in the presence and in the absence of BibA protein followed by the addition of a mouse α-BibA polyclonal antibody. The ME180 cervical cells were then stained with FITC-conjugated α-mouse IgG secondary antibody. A positive control was obtained by treating the ME180 cervical cells only with the FITC-conjugated α-mouse IgG secondary antibody (*i.e.*, in the absence of mouse α-BibA polyclonal antibody). The analysis was repeated with Caco2 intestinal cells, A549 alveolar cells, and 16HBE140 bronchial cells. As negative control we used GBS7 protein, which was cloned identically to BibA.

[292] BibA binding, expressed as Dmean channel values, was measured by FACScan cytometer as difference in fluorescence intensity between cell incubated with or without BibA. Results are shown in **FIG. 12**. The "secondary antibody only" area indicates cells treated with FITC-conjugated antibody alone. BibA binding, expressed as Dmean channel values, was measured by FACScan cytometer as difference in fluorescence intensity between cell incubated with or without BibA. As negative control we used GBS7 protein, which was cloned identically to BibA.

EXAMPLE 9

BibA binds to the surface of epithelial cells by the proline-rich motif

[293] Epithelial cells were incubated in the presence of biotinylated BibA protein or biotinylated BibA fragments and then stained with FITC-conjugated streptavidin. The purple area indicates cells treated with FITC-conjugated streptavidin alone. BibA binding, expressed as Delta mean channel values, was measured by a FACScan cytometer as the difference in fluorescence intensity between cells incubated with or without proteins.

[294] The results are shown in **FIG. 13**. These findings demonstrate that BibA binds to the surface of epithelial cells by the proline-rich motif. See also **FIGS. 25A** and **25B**; **FIG. 26**.

EXAMPLE 10

Purified human-IgG binds to BibA protein

[295] Purified GBS3-His, GBS3-Nt-His (Nt), GBS3-Nt1-His (Nt1), GBS3-T-His (T), GBS3-Ct-His (Ct), GBS M protein (M1) (positive control) and GBS104 (negative control) were separated on SDS-4%-12%PAGE gel (200V) and transferred to nitrocellulose membrane (35V, 1hr, 15min). The nitrocellulose membrane was blocked for 1 hr at RT with 5%Milk-PBS-0,1% Tween20 (PBS-T) and overlaid with immunoglobulins (human-IgA or human-IgG) in PBS-T for 1hr at RT. The membrane was washed three times with PBS-T, overlaid with secondary HRP conjugated antibodies (1:1000) in 5%Milk-PBS-0,1% Tween20, and washed three times with PBS-T. Positive binding to immunoglobulins was detected using an ECL™ substrate.

[296] The results are shown in **FIG. 14**. The results demonstrate that the full-length protein and fragments of the protein bind to human IgG with different affinities.

EXAMPLE 11

BibA-His is specific for human and rabbit IgG

[297] BibA-His was separated on SDS-PAGE and then transferred to a nitrocellulose membrane. After blocking, the membranes were incubated with serum of different species and then probed with anti-IgG antibody conjugated with HRP. The proteins were revealed with a colorimetric kit.

[298] The results are shown in **FIG. 17** and **Table 1**. These results demonstrate that BibA-His is specific for human and rabbit IgG and does not bind mouse IgG.

EXAMPLE 12

Purified human-IgA binds to BibA protein

[299] Purified BibA-His, BibA-Nt-His (Nt), BibA-Nt1-His (Nt1), BibA-T-His (T), BibA-Ct-His (Ct), GBS M protein (M1) (positive control) and GBS104 (negative control) were separated on SDS-4%-12%PAGE gel (200V) and transferred to nitrocellulose membrane (35V, 1hr, 15min). The nitrocellulose membrane was blocked for 1 hr at RT with 5%Milk-PBS-0,1% Tween20 (PBS-T) and overlaid with human-IgA-HRP conjugated in PBS-T for 1hr at RT. The membrane was washed three times with PBS-T. Positive binding to immunoglobulins was detected using an ECL™ substrate.The protein was blocked by incubating the membrane with 5% milk-PBS-T for 1 hr at RT. The membrane was incubated with human IgG-HRP (5 μg/ml) in PBS-T for 1.5 hr, then washed three times with PBS-T. Positive binding to immunoglobulins was detected using an ECL™ substrate (PIERCE kit: SuperSignal West Pico Chemiluminescent Substrate) and 4-CN kit (BIO-RAD).

[300] Native BibA protein and portions of BibA were examined via dot blot.

[301] The results are shown in **FIG. 15** and **Table 2**. These results demonstrate that the N-terminal portion of BibA binds to purified human IgA.

[302] BibA-His and BibA fragments were digested with trypsin for 15 minutes and separated on SDS-PAGE gel. An overlay with h-IgA-HRP (1 ml/ml) was performed on the proteins transferring on nitrocellulose membrane. The results are shown in **FIG. 16**. Tryptic digestion produces a fragment of 32kDa which still binds h-IgA.

[303] Human-IgA-FITC binding to the surface of 2603-BibA overexpressing mutant strain is shown in **FIG. 9**. FACS analysis revealed an increment of IgA binding to the surface of BibA overexpressing mutants.

EXAMPLE 13

Production of complete and truncated forms of BibA

Plasmids encoding complete or truncated form of BibA proteins were constructed as follows. Domains of BibA were amplified by PCR using 2603 genome as the template. The oligonucleotide primers used are listed in the Table 1. Forward primers all contained NdeI restriction sites. The reverse primers all contained XhoI restriction sites. PCR product were digested with NdeI and XhoI, gel purified and ligated with NdeI and XhoI restricted pET21b(+). All constructs were verified by DNA sequencing. The recombinant proteins were expressed His-tag proteins.

GBS3-His is the entire form of BibA (GBS3)

GBS3-Nt-His is the coiled-coil domain of BibA

GBS3-Nt1-His is the coiled-coil domain without the first 180 aa

GBS3-Ct-His is the proline-rich domain of BibA

GBS3-Nt3-His contained the proline-rich domain and a portion of coiled-coil domain

GBS3-T-His contained the first 180 aa

GBS3-His
from 34aa to 609aa

Forward NdeI 5′-GGAATTCCATATG**CACGCGGATACTAGTTCAGGA**-3′
(SEQ ID NO:20)
Reverse XhoI 5′-CCCGCTCGAG***AATTGCTAAGAGTGGACTTGC***-3′
(SEQ ID NO:21)

Nucleotide sequence (SEQ ID NO:22)

CACGCGGATACTAGTTCAGGAATATCGGCTTCAATTCCTCATAAGAAACAAGTTAATTTAGGGG
CGGTTACTCTGAAGAATTTGATTTCTAAATATCGTGGTAATGACAAAGCTATTGCTATACTTTT

AAGTAGAGTAAATGATTTTAATAGAGCATCACAGGATACACTTCCACAATTAATTAATAGTACT
GAAGCAGAAATTAGAAATATTTTATATCAAGGACAAATTGGTAAGCAAAATAAACCAAGTGTAA
CTACACATGCTAAAGTTAGTGATCAAGAACTAGGTAAGCAGTCAAGACGTTCTCAAGATATCAT
TAAGTCATTAGGTTTCCTTTCATCAGACCAAAAAGATATTTTAGTTAAATCTATTAGCTCTTCA
AAAGATTCGCAACTTATTCTTAAATTTGTAACTCAAGCCACGCAACTGAATAATGCTGAATCAA
CAAAAGCTAAGCAAATGGCTCAAAATGACGTGGCCTTAATAAAAAATATAAGCCCCGAAGTCTT
AGAAGAATATAAAGAAAAAATTCAAAGAGCTAGCACTAAGAGTCAAGTTGATGAGTTTGTAGCA
GAAGCTAAAAAAGTTGTTAATTCCAATAAAGAAACGTTGGTAAATCAGGCCAATGGTAAAAAGC
AAGAAATTGCTAAGTTAGAAAATTTATCTAACGATGAAATGTTGAGATATAATACTGCAATTGA
TAATGTAGTGAAACAGTATAATGAAGGTAAGCTCAATATTACTGCTGCAATGAATGCTTTAAAT
AGTATTAAGCAAGCAGCACAGGAAGTTGCCCAGAAAAACTTACAAAAGCAGTATGCTAAAAAAA
TTGAAAGAATAAGTTCAAAAGGATTAGCGTTATCTAAAAAGGCTAAAGAAATTTATGAAAAGCA
TAAAAGTATTTTGCCTACACCTGGATATTATGCAGACTCTGTGGGAACTTATTTGAATAGGTTT
AGAGATAAACAAACTTTCGGAAATAGGAGTGTTTGGACTGGTCAAAGTGGACTTGATGAAGCAA
AAAAAATGCTTGATGAAGTCAAAAAGCTTTTAAAAGAACTTCAAGACCTTACCAGAGGTACTAA
AGAAGATAAAAAACCAGACGTTAAGCCAGAAGCCAAACCAGAGGCCAAACCAGACGTTAAGCCA
GAGGCCAAACCAGACGTTAAGCCAGAAGCTAAGCCAGACGTTAAACCAGAAGCTAAGCCAGACG
TTAAACCAGAAGCTAAGCCAGACGTTAAACCAGAAGCTAAGCCAGACGTTAAACCAAAGGCCAA
ACCAGACGTTAAGCCAGAAGCTAAGCCAGACGTTAAACCAGACGTTAAACCAGACGTTAAGCCA
GAGGCCAAACCAGAGGATAAGCCAGACGTTAAACCAGACGTTAAGCCAGAAGCTAAACCAGACG
TTAAGCCAGAGGCCAAACCAGAAGCTAAGCCAGAAGCTAAGCCAGAAGCTAAGCCAGAGGCCAA
ACCAGAAGCTAAGCCAGACGTTAAGCCAGAAGCTAAACCAGACGTTAAACCAGAGGCTAAGCCA
GAAGCTAAACCAGAGGCTAAGTCAGAAGCTAAACCAGAGGCTAAGCTAGAAGCTAAACCAGAGG
CCAAACCAGCAACCAAAAAATCGGTTAATACTAGCGGAAACTTGGCGGCTAAAAAAGCTATTGA
AAACAAAAAGTATAGTAAAAAATTACCATCAACGGGTGAAGCC***GCAAGTCCACTCTTAGCAATT***

Amino acid sequence of the fragment (SEQ ID NO:23)

MetHADTSSGISASIPHKKQVNLGAVTLKNLISKYRGNDKAIAILLSRVNDFNRASQDTLPQLI
NSTEAEIRNILYQGQIGKQNKPSVTTHAKVSDQELGKQSRRSQDIIKSLGFLSSDQKDILVKSI
SSSKDSQLILKFVTQATQLNNAESTKAKQMAQNDVALIKNISPEVLEEYKEKIQRASTKSQVDE
FVAEAKKVVNSNKETLVNQANGKKQEIAKLENLSNDEMLRYNTAIDNVVKQYNEGKLNITAAMN
ALNSIKQAAQEVAQKNLQKQYAKKIERISSKGLALSKKAKEIYEKHKSILPTPGYYADSVGTYL
NRFRDKQTFGNRSVWTGQSGLDEAKKMLDEVKKLLKELQDLTRGTKEDKKPDVKPEAKPEAKPD
VKPEAKPDVKPEAKPDVKPEAKPDVKPEAKPDVKPKAKPDVKPEAKPDVKPDVKPD
VKPEAKPEDKPDVKPDVKPEAKPDVKPEAKPEAKPEAKPEAKPEAKPDVKPEAKPDVKPE
AKPEAKPEAKSEAKPEAKLEAKPEAKPATKKSVNTSGNLAAKKAIENKKYSKKLPSTGEAASPL
LAIVSLIVMLSAGLITLEHHHHHH

GBS3-**Nt-His**
from 34aa to 394aa

Forward NdeI 5′-GGAATTCCATATGCACGCGGATACTAGTTCAGGA-3′
(SEQ ID NO:24)

Reverse XhoI 5′-CCCGCTCGAGACCTCTGGTAAGGTCTTGAA-3′
(SEQ ID NO:25)

Nucleotide sequence (SEQ ID NO:26):

CACGCGGATACTAGTTCAGGAATATCGGCTTCAATTCCTCATAAGAAACAAGTTAATTTAGGGG
CGGTTACTCTGAAGAATTTGATTTCTAAATATCGTGGTAATGACAAAGCTATTGCTATACTTTT
AAGTAGAGTAAATGATTTTAATAGAGCATCACAGGATACACTTCCACAATTAATTAATAGTACT
GAAGCAGAAATTAGAAATATTTTATATCAAGGACAAATTGGTAAGCAAAATAAACCAAGTGTAA
CTACACATGCTAAAGTTAGTGATCAAGAACTAGGTAAGCAGTCAAGACGTTCTCAAGATATCAT
TAAGTCATTAGGTTTCCTTTCATCAGACCAAAAAGATATTTTAGTTAAATCTATTAGCTCTTCA
AAAGATTCGCAACTTATTCTTAAATTTGTAACTCAAGCCACGCAACTGAATAATGCTGAATCAA
CAAAAGCTAAGCAAATGGCTCAAAATGACGTGGCCTTAATAAAAAATATAAGCCCCGAAGTCTT
AGAAGAATATAAAGAAAAAATTCAAAGAGCTAGCACTAAGAGTCAAGTTGATGAGTTTGTAGCA
GAAGCTAAAAAAGTTGTTAATTCCAATAAAGAAACGTTGGTAAATCAGGCCAATGGTAAAAAGC
AAGAAATTGCTAAGTTAGAAAATTTATCTAACGATGAAATGTTGAGATATAATACTGCAATTGA
TAATGTAGTGAAACAGTATAATGAAGGTAAGCTCAATATTACTGCTGCAATGAATGCTTTAAAT
AGTATTAAGCAAGCAGCACAGGAAGTTGCCCAGAAAAACTTACAAAAGCAGTATGCTAAAAAAA
TTGAAAGAATAAGTTCAAAAGGATTAGCGTTATCTAAAAAGGCTAAAGAAATTTATGAAAAGCA
TAAAAGTATTTTGCCTACACCTGGATATTATGCAGACTCTGTGGGAACTTATTTGAATAGGTTT
AGAGATAAACAAACTTTCGGAAATAGGAGTGTTTGGACTGGTCAAAGTGGACTTGATGAAGCAA
AAAAAATGCTTGATGAAGTCAAAAAGCTTTTAAAAGAACTTCAAGACCTTACCAGAGGT

Amino acid sequence of the fragment (SEQ ID NO:27)

MetHADTSSGISASIPHKKQVNLGAVTLKNLISKYRGNDKAIAILLSRVNDFNRASQDTLPQLIN
STEAEIRNILYQGQIGKQNKPSVTTHAKVSDQELGKQSRRSQDIIKSLGFLSSDQKDILVKSISS
SKDSQLILKFVTQATQLNNAESTKAKQMAQNDVALIKNISPEVLEEYKEKIQRASTKSQVDEFVA
EAKKVVNSNKETLVNQANGKKQEIAKLENLSNDEMLRYNTAIDNVVKQYNEGKLNITAAMNALNS
IKQAAQEVAQKNLQKQYAKKIERISSKGLALSKKAKEIYEKHKSILPTPGYYADSVGTYLNRFRD
KQTFGNRSVWTGQSGLDEAKKMLDEVKKLLKELQDLTRGLEHHHHHH

BibA-Nt1-His
from 180aa to 394aa

Forward NdeI 5′-GGAATTCCATATGGCTGAATCAACAAAAGCTA-3′

(SEQ ID NO:28)

Reverse XhoI 5′-CCCGCTCGAGACCTCTGGTAAGGTCTTGAA-3′
SEQ ID NO:29)

Nucleotide sequence (SEQ ID NO:30):

GCTGAATCAACAAAAGCTAAGCAAATGGCTCAAAATGACGTGGCCTTAATAAAAAATATAAGCC
CCGAAGTCTTAGAAGAATATAAAGAAAAAATTCAAAGAGCTAGCACTAAGAGTCAAGTTGATGA
GTTTGTAGCAGAAGCTAAAAAAGTTGTTAATTCCAATAAAGAAACGTTGGTAAATCAGGCCAAT
GGTAAAAAGCAAGAAATTGCTAAGTTAGAAAATTTATCTAACGATGAAATGTTGAGATATAATA
CTGCAATTGATAATGTAGTGAAACAGTATAATGAAGGTAAGCTCAATATTACTGCTGCAATGAA
TGCTTTAAATAGTATTAAGCAAGCAGCACAGGAAGTTGCCCAGAAAAACTTACAAAAGCAGTAT
GCTAAAAAAATTGAAAGAATAAGTTCAAAAGGATTAGCGTTATCTAAAAAGGCTAAAGAAATTT
ATGAAAAGCATAAAAGTATTTTGCCTACACCTGGATATTATGCAGACTCTGTGGGAACTTATTT
GAATAGGTTTAGAGATAAACAAACTTTCGGAAATAGGAGTGTTTGGACTGGTCAAAGTGGACTT
GATGAAGCAAAAAAAATGCTTGATGAAGTCAAAAAGCTTTTAAAAGAACTTCAAGACCTTACCA
GAGGT

Amino acid sequence of the fragment (SEQ ID NO:31)

MetAESTKAKQMAQNDVALIKNISPEVLEEYKEKIQRASTKSQVDEFVAEAKKVVNSNKETLVN
QANGKKQEIAKLENLSNDEMLRYNTAIDNVVKQYNEGKLNITAAMNALNSIKQAAQEVAQKNLQ
KQYAKKIERISSKGLALSKKAKEIYEKHKSILPTPGYYADSVGTYLNRFRDKQTFGNRSVWTGQ
SGLDEAKKMLDEVKKLLKELQDLTRGLEHHHHHH

GBS3-Ct-His
from 389aa to 622aa

Forward NdeI 5′-GGAATTCCATATGCCAGACCTTACCAGAGGT-3′
(SEQ ID NO:32)

Reverse XhoI 5′-CCCGCTCGAGCGTAATAAGACCTGCACTT-3′
(SEQ ID NO:33)

Nucleotide sequence (SEQ ID NO:34):

CAAGACCTTACCAGAGGTACTAAAGAAGATAAAAAACCAGACGTTAAGCCAGAAGCCAAACCAG
AGGCCAAACCAGACGTTAAGCCAGAGGCCAAACCAGACGTTAAGCCAGAAGCTAAGCCAGACGT
TAAACCAGAAGCTAAGCCAGACGTTAAACCAGAAGCTAAGCCAGACGTTAAACCAGAAGCTAAG
CCAGACGTTAAACCAAAGGCCAAACCAGACGTTAAGCCAGAAGCTAAGCCAGACGTTAAACCAG
ACGTTAAACCAGACGTTAAGCCAGAGGCCAAACCAGAGGATAAGCCAGACGTTAAACCAGACGT
TAAGCCAGAAGCTAAACCAGACGTTAAGCCAGAGGCCAAACCAGAAGCTAAGCCAGAAGCTAAG

CCAGAAGCTAAGCCAGAGGCCAAACCAGAAGCTAAGCCAGACGTTAAGCCAGAAGCTAAACCAG
ACGTTAAACCAGAGGCTAAGCCAGAAGCTAAACCAGAGGCTAAGTCAGAAGCTAAACCAGAGGC
TAAGCTAGAAGCTAAACCAGAGGCCAAACCAGCAACCAAAAAATCGGTTAATACTAGCGGAAAC
TTGGCGGCTAAAAAAGCTATTGAAAACAAAAAGTATAGTAAAAAATTACCATCAACGGGTGAAG
CCGCAAGTCCACTCTTAGCAATTGTATCACTAATTGTTATGTTAAGTGCAGGTCTTATTACG

Amino acid sequence of the fragment (SEQ ID NO:35)

MetQDLTRGTKEDKKPDVKPEAKPEAKPDVKPEAKPDVKPEAKPDVKPEAKPDVKPEAKPDVKP
EAKPDVKPKAKPDVKPEAKPDVKPDVKPDVKPEAKPEDKPDVKPDVKPEAKPDVKPEAKPEAKP
EAKPEAKPEAKPEAKPDVKPEAKPDVKPEAKPEAKPEAKSEAKPEAKLEAKPEAKPATKKSVNT
SGNLAAKKAIENKKYSKKLPSTGEAASPLLAIVSLIVMLSAGLITLEHHHHHH

GBS3-Nt3-His
From 180aa to 622aa

Primer 7 (SEQ ID NO:36) NdeI 5′-GGAATTCCATATGGCTGAATCAACAAAAGCTA-3′

Primer 9 (SEQ ID NO:37) XhoI 5′-CCCGCTCGAGCGTAATAAGACCTGCACTT-3′

Nucleotide sequence (SEQ ID NO:38):

GCTGAATCAACAAAAGCTAAGCAAATGGCTCAAAATGACGTGGCCTTAATAAAAAATATAAGCC
CCGAAGTCTTAGAAGAATATAAAGAAAAAATTCAAAGAGCTAGCACTAAGAGTCAAGTTGATGA
GTTTGTAGCAGAAGCTAAAAAAGTTGTTAATTCCAATAAAGAAACGTTGGTAAATCAGGCCAAT
GGTAAAAAGCAAGAAATTGCTAAGTTAGAAAATTTATCTAACGATGAAATGTTGAGATATAATA
CTGCAATTGATAATGTAGTGAAACAGTATAATGAAGGTAAGCTCAATATTACTGCTGCAATGAA
TGCTTTAAATAGTATTAAGCAAGCAGCACAGGAAGTTGCCCAGAAAAACTTACAAAAGCAGTAT
GCTAAAAAAATTGAAAGAATAAGTTCAAAAGGATTAGCGTTATCTAAAAAGGCTAAAGAAATTT
ATGAAAAGCATAAAAGTATTTTGCCTACACCTGGATATTATGCAGACTCTGTGGGAACTTATTT
GAATAGGTTTAGAGATAAACAAACTTTCGGAAATAGGAGTGTTTGGACTGGTCAAAGTGGACTT
GATGAAGCAAAAAAAATGCTTGATGAAGTCAAAAAGCTTTTAAAAGAACTTCAAGACCTTACCA
GAGGTACTAAAGAAGATAAAAAACCAGACGTTAAGCCAGAAGCCAAACCAGAGGCCAAACCAGA
CGTTAAGCCAGAGGCCAAACCAGACGTTAAGCCAGAAGCTAAGCCAGACGTTAAACCAGAAGCT
AAGCCAGACGTTAAACCAGAAGCTAAGCCAGACGTTAAACCAGAAGCTAAGCCAGACGTTAAAC
CAAAGGCCAAACCAGACGTTAAGCCAGAAGCTAAGCCAGACGTTAAACCAGACGTTAAACCAGA
CGTTAAGCCAGAGGCCAAACCAGAGGATAAGCCAGACGTTAAACCAGACGTTAAGCCAGAAGCT
AAACCAGACGTTAAGCCAGAGGCCAAACCAGAAGCTAAGCCAGAAGCTAAGCCAGAAGCTAAGC
CAGAGGCCAAACCAGAAGCTAAGCCAGACGTTAAGCCAGAAGCTAAACCAGACGTTAAACCAGA
GGCTAAGCCAGAAGCTAAACCAGAGGCTAAGTCAGAAGCTAAACCAGAGGCTAAGCTAGAAGCT
AAACCAGAGGCCAAACCAGCAACCAAAAAATCGGTTAATACTAGCGGAAACTTGGCGGCTAAAA

AAGCTATTGAAAACAAAAAGTATAGTAAAAAATTACCATCAACGGGTGAAGCCGCAAGTCCACT
CTTAGCAATTGTATCACTAATTGTTATGTTAAGTGCAGGTCTTATTACG

Amino acid sequence of the fragment (SEQ ID NO:39):

MetAESTKAKQMAQNDVALIKNISPEVLEEYKEKIQRASTKSQVDEFVAEAKKVVNSNKETLVN
QANGKKQEIAKLENLSNDEMLRYNTAIDNVVKQYNEGKLNITAAMNALNSIKQAAQEVAQKNLQ
KQYAKKIERISSKGLALSKKAKEIYEKHKSILPTPGYYADSVGTYLNRFRDKQTFGNRSVWTGQ
SGLDEAKKMLDEVKKLLKELQDLTRGTKEDKKPDVKPEAKPEAKPDVKPEAKPDVKPEAKPDVK
PEAKPDVKPEAKPDVKPKAKPDVKPEAKPDVKPDVKPDVKPEAKPEDKPDVKPDVK
PEAKPDVKPEAKPEAKPEAKPEAKPEAKPDVKPEAKPDVKPEAKPEAKPEAKSEAKPEAK
LEAKPEAKPATKKSVNTSGNLAAKKAIENKKYSKKLPSTGEAASPLLAIVSLIVMLSAGLITLE
HHHHHH

GBS3-T-His

Primer 1 NdeI 5′-GGAATTCCATATGCACGCGGATACTAGTTCAGGA-3′
(SEQ ID NO:40)

GBS3-T-Rev XhoI 5′-CCCGCTCGAGATTATTCAGTTGCGTGGCTTGAGT-3′
(SEQ ID NO:41)

Nucleotide sequence (SEQ ID NO:42):

CACGCGGATACTAGTTCAGGAATATCGGCTTCAATTCCTCATAAGAAACAAGTTAATTTAGGGG
CGGTTACTCTGAAGAATTTGATTTCTAAATATCGTGGTAATGACAAAGCTATTGCTATACTTTT
AAGTAGAGTAAATGATTTTAATAGAGCATCACAGGATACACTTCCACAATTAATTAATAGTACT
GAAGCAGAAATTAGAAATATTTTATATCAAGGACAAATTGGTAAGCAAAATAAACCAAGTGTAA
CTACACATGCTAAAGTTAGTGATCAAGAACTAGGTAAGCAGTCAAGACGTTCTCAAGATATCAT
TAAGTCATTAGGTTTCCTTTCATCAGACCAAAAAGATATTTTAGTTAAATCTATTAGCTCTTCA
AAAGATTCGCAACTTATTCTTAAATTTGTA**ACT**CAAGCCACGCAACTGAATAAT

Amino acid sequence of the fragment (SEQ ID NO:43):

MetHADTSSGISASIPHKKQVNLGAVTLKNLISKYRGNDKAIAILLSRVNDFNRASQDTLPQLIN
STEAEIRNILYQGQIGKQNKPSVTTHAKVSDQELGKQSRRSQDIIKSLGFLSSDQKDILVKSISS
SKDSQLILKFVTQATQLNNLEHHHHHH

EXAMPLE 14

Experimental procedures

Cell culture

[304] The human cervical epithelial cell line ME180 was purchased from the American Type Culture Collection (ATCC, Rockville, Md.). ME180 cells were maintained in RPMI 1640 medium with 10% heat-inactivated fetal bovine serum (FBS). The lung carcinoma cell line A549 (type II alveolar epithelial cells) and the colon carcinoma epithelial cell line Caco2 also were supplied by the ATCC and were grown in DMEM supplemented with 10% FBS, 4.5g/L glucose and non-essential amino acids. The human bronchial epithelial cell line 16HBE14, which is transformed with SV40 large T antigen (Grifantini *et al.*, 2002), was cultured in DMEM supplemented with 10% FBS, 1.5 mM glutamine, and 100 µg/ml kanamycin sulfate.

Bacterial strains and growth conditions

[305] *S. agalactiae strains* 2603 V/R and 515 Ia were used in this study. To determine BibA protein conservation, we analyzed a panel of *S. agalactiae* strains. *E. coli* DH5α and DH10BT1 were used for cloning purposes and *E. coli* BL21 (DE3) for expression of BibA fusion protein. *S. agalactiae* was cultivated at 37°C in Todd-Hewitt broth (THB) up to OD600 0.4. *S. agalactiae* strains carrying the plasmid pAM401bibA were grown in the presence of cloramphenicol (10 µg/ml). *E. coli* was grown in Luria broth. *E. coli* clones carrying the plasmids pAM401bibA, pJRS233ΔbibA or pET21(b)+ derivatives were grown in the presence of cloramphenicol (20 µg/ml), erythromycin (400 µg/ml) or ampicillin (100 µg/ml), respectively.

Construction of 2603 V/R bibA deletion mutant

[306] The *bibA* gene was deleted in *S. agalactiae* strain 2603 V/R according to the procedure described in Lauer *et al.*, 2005. The in-frame deletion fragment was obtained by Splicing

Overlap Extension (SOE) PCR using the primers 5′-CCCG***CTCGAG***ACTAGTGACAAACCTTGGAAT-3′ (SEQ ID NO:44), 5′-GTCAGCACGGTTTGCCATAAACCGAAAGGTCTATCC-3′ (SEQ ID NO:45), 5′-ACCTTTCGGTTTATGGCAAACGCTGCTGACATTG-3′ (SEQ ID NO:46) and 5′-CCCG***CTCGAG***ACAGATAAGCCTAAGCGACTT-3′ (SEQ ID NO:47). The XhoI restriction enzyme cleavage sites were incorporated at the 5′-end of the primer (bold and italicized) to clone the fragment into the XhoI-digested pJRS233 plasmid. After cloning the in frame deletion fragment in the pJRS233, the plasmid pJRS233Δ*bibA* was obtained.

[307] The plasmid pJRS233Δ*bibA* was then transformed into the 2603 V/R strain by electroporation and transformants were selected after growth at 30°C on agar plates containing 1μg/ml erythromycin. Transformants were then grown at 37°C with erythromycin selection as described in Maguin *et al*., 1996. Integrant strains were serially passaged for 5 days in liquid medium at 30°C without erythromycin selection to facilitate the excision of plasmid pJRS233Δ*bibA*, resulting in the bibA deletion on the chromosome. Dilutions of the serially passaged cultures were plated onto agar plates, and single colonies were tested for erythromycin sensitivity to confirm the excision of pJRS233Δ*bibA*.

Plasmid-mediated expression of BibA in S. agalactiae

[308] The *bibA* gene including its own promoter and terminator was amplified by PCR from chromosomal DNA of *S. agalactiae* 2603 V/R using primers 5′-CCCCGCC***GGGATCC***CCAACCCTTATCAAAAGA-3′ (SEQ ID NO:48) and 5′-CTCTGCATG***GTCGAC***ATAGAAACAACCCAAACCC-3′ (SEQ ID NO:49). The restriction enzymes cleavage sites *Bam*HI and *Sal*I were incorporated at the 5′-ends of the primers (bold and italicized) to clone the PCR product into the BamHI/SalI digested *E. coli-Streptococcus* pAM401 expression construct. The plasmid pAM401*bibA* was obtained by cloning the *bibA* gene into pAM401. Plasmid pAM401*bibA* was transformed

by electroporation into 2603 V/R and 515 Ia strains with subsequent cloramphenicol selection.

BibA recombinant protein expression and purification

[309] In order to express the recombinant form of BibA, the open reading frame of the *bibA* gene from *S. agalactiae* 2603 was used as a template. The construct was amplified by PCR using specific primers, which introduced *Nde*I and *Xho*I restriction enzyme sites:

5′-GGAATTCCATATGCACGCG GATACTAGTTCAGGA-3′ (SEQ ID NO:50) and

5′-CCCGCTCGAGAATTGCTAAGAGTGG ACTTGC-3′ (SEQ ID NO:51).

[310] In the case of BibA N-terminal construct (aa 34-394) the following amplification primers were used:

5′-GGAATTCCATATGCACGCGGATACTAGTTCAGGA-3′ (SEQ ID NO:52) and

5′-CCC GCTCGAGACCTCTGGTAAGGTCTTGAA-3′ (SEQ ID NO:53).

[311] For BibA C-terminal construct (aa 389-622) the following primers were used:

5′-GGAATTCCATATGCCAGACCTTACCAGAGGT-3′ (SEQ ID NO:54) and

5′-CCCGCTCGAGCGTAATAAGACC TGCACTT-3′ (SEQ ID NO:55).

[312] The PCR products were cloned into the pET21(b)+ vector, which was used to transform *E. coli* BL21 (DE3) cells. BL21 (DE3) cells were grown in LB-Amp (100 μg/ml ampicillin) and induced with IPTG at final concentration of 1 mM for 3 hours. The resulting biomass was suspended in 0.3M NaCl, 50 mM Na-PO4 buffer, pH 8.0, and cells were lysed by two passages at 18,000 psi using a Basic Z Model Cell Disrupter (Constant Systems Ltd., Daventry, UK). The sample was then loaded onto a His-Trap Ni-Activated Chelating Sepharose FF column (Amersham Biosciences, Milan, Italy) at a flow rate of 5 ml/min. Bound proteins were then eluted from the column by running a gradient from 0

to 50% of 500 mM Imidazole, 0.3 M NaCl, 50 mM Na phosphate buffer, pH 8.0 in 12 CV. The IMAC (Immobilized Metal Affinity Column) eluted material was collected in 2.5-ml fractions, and the fractions containing the BibA-His protein were pooled. The collected pools were then loaded onto a HiLoad 26/60 Superdex 200 gel filtration column (Amersham Biosciences, Milan, Italy). The protein was eluted isocratically at 2.5 ml/min flow rate collecting 2.5-ml fractions.

Bacterial extracts

[313] GBS protein extracts were prepared by growing bacteria up to OD_{600} 0.4. The resulting pellet washed in PBS and incubated for 1hr at 37°C in 500 µl of Tris-HCl 50mM (pH6.8) containing protease inhibitors and 400 U/ml of mutanolysin (SIGMA, MO, USA). T he bacterial suspension was then pelleted and supernatants containing peptidoglycan-associated proteins were used for Western blotting analyis of BibA. In order to prepare GBS extracts containing the secreted protein fraction, supernatant of bacteria cultures grown to OD_{600} 0.4 were collected and directly used in PAGE.

Fluorescence-activated cell sorter analysis

[314] In order to quantify the exposure of BibA on bacterial surface, GBS was grown up to OD600 0.4 and incubated with rabbit anti-BibA serum or rabbit anti-PBS serum (negative control) in 0.1% BSA plus 20% of normal calf serum (NCS) for 1 hr at 4°C. Bacteria were then washed in PBS containing 0.1% BSA and incubated with phicoerytrin (PE)-conjugated secondary antibodies (Jackson Immuno Research Inc., PA, USA) for 45 min at 4°C. After washing, bacteria were fixed with 2% PFA for 20 min at RT, resuspended in 200 µl of PBS, and analyzed by a FACSscan flow cytometer (Becton Dickinson) using the Cell Quest software program from Becton Dickinson.

[315] In the binding assay, ME180 or A549 cells were mixed with different concentrations of BibA and incubated for 1 hr at 4°C. Cells were subsequently incubated for 45 min. at 4°C with rabbit anti-BibA serum in 5% FCS. Cells were then washed twice in PBS and

incubated for 45 min. at 4°C with the PE-conjugated secondary antibodies. Cell-bound fluorescence was analyzed with a FACS using the Cell Quest program. MFI values of cells incubated with or without protein were compared.

Association assay

[316] ME180 and A549 epithelial cells were infected with approximately 10 bacteria/cell in infection medium (basal medium without antibiotics) supplemented with 2% FBS in 200µl volumes. At the end of a 3-hour incubation at 37□C in 5% CO2 (v/v), total colony-forming units (c.f.u.) were estimated after addition of 1% saponin to the wells contents. Adhesiveness was quantified by determining the ratio of cell-associated c.f.u. versus total c.f.u. present in the assay.

Immunogold labeling and electron microscopy

[317] GBS strains 2603 V/R, 2603Δ*bibA*, 515 Ia and 515pAM401*bibA* were grown overnight in THB medium (10 ml). Bacterial cells from 1 ml of the overnight culture were resuspended in 5ml of fresh THB medium and grown at 37°C up to OD 0.3 (exponential phase). Bacteria were then centrifuged for 10min at 3000 rpm (RT), washed and resuspended in 1ml of PBS. Formvar-carbon-coated nickel grids were floated on drops of GBS suspensions for 5min. The grids were then fixed in 2% PFA for 5 min, and placed in blocking solution (PBS containing 1% normal rabbit serum and 1% BSA) for 30 min. The grids were then floated on drops of primary antiserum against the BibA protein diluted 1:20 in blocking solution for 30min at RT, washed with six drops of blocking solution, and floated on secondary antibody conjugated to 10-nm gold particles diluted 1:10 in 1% BSA for 30 min. The grids were examined by using a TEM GEOL 1200EX II transmission electron microscope.

Confocal immunofluorescence microscopy

[318] A549 cells were grown to confluence in a Lab-TekII Chamber Slide System (Nalgene) in 1 ml of DMEM supplemented with 10% FBS, 4.5 g/L glucose and non-essential amino

acids. Cells were then infected with bacteria at a MOI 10:1 and incubated at 37°C for 2 hr. Cells were then fixed in 2% paraformaldehyde for 30 min at room temperature (RT) or at 4°C overnight. After fixing, the monolayers were blocked with 3% BSA and incubated for 1hr at RT with a mix of mouse anti-capsule and rabbit anti-BibA polyclonal antibodies diluted in 1% BSA. Bacteria were then stained, for 1hr at RT, with goat anti-mouse and anti-rabbit Alexa fluor (Molecular Probes) conjugated antibodies (excitation at 568nm and 488nm, respectively). F-actin was stained with Alexa Fluor 622 conjugated phalloidin. The chamber walls were then removed from the glass slide. A Slow Fade reagent kit (Molecular Probes) used to mount cover slips. The slides were viewed with a Bio-Rad confocal scanning microscope.

Dot blot and Western blot analyses

[319] In dot blot analysis, purified recombinant BibA protein (range ~2 μg-0.01μg) was absorbed to a nitrocellulose membrane by using a BIORAD dot blot system. After saturation with 5% milk, the membrane was incubated with 0.5 μg/ml of serum purified human-IgA (Pierce) or human IgG (SIGMA). After washing, the membrane was incubated with HRP-conjugated rabbit anti-human IgA (Dako) or HRP-conjugated goat anti-human IgG (BD) and positive binding detected by ECL.

[320] The same protocol was used to test the binding of BibA to C4BP. Purified C4BP derived from citrated human plasma was purchased from Kordia Life Science, (Leiden, ND)., Mouse monoclonal anti-C4BP antibodies (BIOTREND Chemikalien GmbH, Köln) were used to reveal C4BP binding to BibA.

[321] Western blot analysis of BibA binding to Ig or C4BP was performed by transferring SDS-PAGE separated proteins to nitrocellulose membranes (Portran). Membranes were then blocked in 5% milk and overlaid for 1 hr with 5 μg/ml of (a) purified IgG from normal human serum (SIGMA); (b) purified IgG from normal mouse serum (SIGMA); c) purified IgG from bovine serum (SIGMA); d) purified IgA from human serum (Pierce); (e) purified IgA from human colostrums (SIGMA); or (f) human plasma C4BP (Kordia

Life Science, ND). After washing, membranes were incubated with the respective HRP-conjugated secondary antibodies, and detection was performed by ECL.

Sequence analysis

[322] The alignment of 2603 V/R (GenBank Accession Number NP_689049; SEQ ID NO:56), 18RS21 (AAJO00000000; SEQ ID NO:57), 515 Ia (AAJP00000000; SEQ ID NO:58), NEM316 (NP_736451; SEQ ID NO:59), H36B (AAJS00000000; SEQ ID NO:60), CJB111 (AAJQ00000000; SEQ ID NO:61), A909 (YP_330593; SEQ ID NO:62; see also SEQ ID NO:67) and COH1 (AAJR00000000; SEQ ID NO:63) strains was performed using ClustalW (Thompson *et al.*, 1994).

EXAMPLE 15

Additional evidence that BibA is exposed on GBS *surface*

[323] As shown in **FIG. 19A**, FACS analysis of 2603 V/R strain grown at exponential phase (OD_{600}=0.35) revealed a shift in bacterial fluorescence after staining with anti-BibA antibody. This indicated that BibA is exposed on GBS surface. This finding was further confirmed by transmission immuno-electron microscopy (IEM) showing positive immunogold labeling of BibA on 2603 V/R surface (**FIG. 19B**). Western blot analysis of 2603 V/R bacterial extracts showed the presence of a single band recognized by anti-BibA antibodies in both peptidoglycan-associated protein fraction and bacteria supernatants (**FIG. 19C**). The band identified as BibA has an apparent MW of ≈ 80kD (**FIG. 19C**), compared to the expected MW of 66kD. We believe that the presence of a prolin-rich motif in the C-terminal region of BibA is responsible for such a discrepancy. Indeed, it is known that prolin-rich regions may retard protein electrophoretic migration (Hollingshead *et al.*, 1986). Comparative analysis of bacteria grown at exponential or stationary phases revealed no differences in the expression of BibA as surface exposed or secreted protein (data not shown). As expected, BibA knockout mutant strain showed nor

BibA FACS positive fluorescence neither immunogold surface labeling (**FIGS. 19D** and **19E**).

[324] In order to demonstrate that the anchoring of BibA to the cell wall was due to the presence of the LPXTG (SEQ ID NO:3) motif, we investigated BibA surface exposure in the strain 515 Ia, in which, due to a frameshift, the protein is lacking the LPXTG (SEQ ID NO:3) motif and therefore is predicted to be expressed in a truncated form (Tettelin *et al.*, 2005). Both FACS analysis and IEM confirmed that in such a strain BibA was not surface exposed (**FIG. 19E** and **19F**). Moreover, Western blot analysis showed that BibA was found in 515 Ia bacterial supernatant, but not in the peptidoglycan associated fraction (**FIG. 19G**). The apparent molecular weight of 38kD is in agreement with the predicted truncated form. When we introduced in the strain 515 Ia a plasmid carrying the 2603 V/R region containing the *bibA* gene and its regulatory elements (pAM401*bibA*), BibA was translocated and anchored on the bacterial surface, as demonstrated by Western blotting, FACS and IEM analysis (**FIGS. 19H, 19I and 19L**).

EXAMPLE 16

BibA specifically binds to human immunoglobulins

[325] Because sequence analysis of BibA indicated some similarity with streptococcal immunoglobulin-binding proteins, we performed Western blotting analysis of recombinant BibA overlaid with purified serum-derived immunoglobulins (Ig). Experimental positive control was the M1 protein of GBS, which is an IgG and IgA binding protein (Cunningham, 2000). The recently reported GBS pilus component protein GBS104 (Lauer *et al.*, 2005) was used as unrelated negative control. As shown in **FIG. 20A**, BibA specifically bound to purified human serum IgG, but not to mouse or bovine IgG. On the other hand, M1 protein reacted with human, mouse and bovine IgG isoforms at similar levels.

[326] BibA binding to purified human serum- or secretory colostrums-derived IgA was also tested. As for the M1 protein, BibA positively recognizes both serum-derived and secretory IgA (**FIG. 20B**). In order to demonstrate that the binding properties were not due to the gel denaturing conditions, we performed native dot-blot experiments. Recombinant BibA protein was serially diluted on nitrocellulose membrane and probed with 0.5 μg/ml purified human serum IgG and IgA. As shown in **FIGS. 20C** and **20D**, probing of native BibA with Ig confirmed the binding to human IgG and IgA. The reactivity of BibA for human IgA appeared to be stronger than that for human IgG. Indeed, a positive binding to IgA was already observed at a concentration of BibA of 0.4 μg, while for IgG the concentration of BibA necessary to the binding was of 1.0 μg (**FIG. 20D**). On the contrary, a strong binding to IgG was detected only up BibA (**FIG. 20C**).

[327] In order to elucidate the BibA binding regiong to Ig, we generated two constructs comprising the N-terminal portion of BibA (aa 34-394) or the C-terminal (aa 400-600). These two BibA constructs have been tested for binding to human IgG and IgA in overlay immunoblotting assays. As shown in **FIG. 20E**, BibA binding to human IgG resided prevalently in the N-terminal region of the protein, although some binding was observed also associated to the C-terminal portion. On the other hand, the binding to human IgA was exclusively associated to the N-terminal portion of BibA (**FIG. 20F**).

EXAMPLE 17

BibA binds to human complement regulator C4bp

[328] Because both BibA and M proteins bind to human IgA, we asked if the previously described (Carlsson *et al.*, 2003) ability of M proteins to bind C4b-binding protein (C4bp) was also carried by BibA. We tested BibA binding activity by C4bp overlay blots in both denaturing and non-denaturing conditions. As shown in **FIG. 21**, recombinant BibA separated in SDS-gel electrophoresis (**FIG. 21A**) or spotted in the native form on nitrocellulose membrane (**FIG. 21B**) highly reacts with C4bp overlaid at 5 μg/ml. M1 similarly bound to C4bp in both conditions, while a negative control protein (GBS201),

randomly chosen from the 2603 V/R genome, did not bind. Of interest, BibA did not show any binding for the alternative complement pathway regulator Factor H. BibA N-terminal and C-terminal constructs were also tested for C4bp binding. As shown in **FIG. 21C**, overlay blots of SDS-PAGE separated BibA showed that the N-terminal region of the protein was sufficient to specifically bind to C4bp. No binding was observed by the C-terminal portion.

EXAMPLE 18

BibA recombinant protein binds to epithelial cells

[329] *In silico* prediction of BibA propensity to form colied-coil regions suggested an adhesive phenotype. We initially tested the capacity of the recombinant BibA, as expressed in the 2603 V/R strain, to bind to ME180 cervical epithelial cells. BibA binding was performed by incubating cells with different concentrations of the recombinant protein for 1h at 4°C. A rabbit polyclonal serum raised against recombinant BibA was used as primary antibody and the binding detected by R-Phycoerythrin-conjugated secondary antibody. To determine antibody unspecific binding, cells were incubated with primary polyclonal antibodies in the absence of the protein. After incubation of ME180 cells with increased concentrations of BibA, we found that the binding of BibA reached a plateau at a concentration of ≈ 5 μg/ml.

[330] As shown in **FIG. 22A**, because the binding of BibA to ME180 cells could be saturated, the affinity of recombinant BibA for its putative receptor was estimated by plotting the mean of fluorescence intensity of the BibA-receptor complex versus the free BibA concentration (**FIG. 22B**). The Kd value was then calculated as the BibA concentration that determines the saturation of 50% of the putative receptors present on cells and evaluated to be in the order of $\approx 4x10^{-8}$ M.. We also tested binding of recombinant BibA to intestinal (Caco2), pulmonary (A549) and bronchial (16HBE) epithelial cell lines. Incubation of these cells with 10 μg/ml of recombinant BibA significantly increased the

mean of fluorescence of the BibA-receptor complex (**FIG. 22C**), even if the intensity of the shift varied among the different cell types.

EXAMPLE 19

BibA is involved in GBS *adhesion to epithelial cells*

[331] In order to confirm that recombinant BibA adhesive properties were associated to a functional role during interaction with epithelial cells, we performed association assays comparing the 2603 V/R wild type strain to the isogenic BibA knockout mutant strain, which does not express the protein on the bacterial surface (**FIG. 19D**). As shown in FIG. 23A and B, the absence of BibA on the surface of 2603 V/R strain significantly reduced GBS capacity to associate to both ME180 and A549 cells ($p<0.05$). Complementation of the mutation by inserting the pAM401*bibA* plasmid restored the adhesive phenotype (data not shown). The impaired capacity of the 2603Δ*bibA* strain to adhere to epithelial cells was also evident in confocal imaging experiments. 2603 V/R wild type strain and the isogenic BibA knockout mutant strain were stained with rabbit anti-BibA and mouse anti-serotype V polyclonal antibodies.

[332] As shown in **FIGS. 23C** and **23D**, the number of bacteria associated to epithelial cells found in a microscopy field (magnification 20x) was reduced in the BibA mutant strain. These results were in total agreement with those obtained by association assay. Transformation of the 2603 V/R wild type strain with the pAM401*bibA* plasmid was used as a tool to increase, BibA exposure on bacterial surface. FACS experiments confirmed that the 2603 pAM401*bibA* strain showed a 30% increase in the number of fluorescence intensity channels compared to the wild type strain. Association assays demonstrated that BibA overexpression was functionally related to the capacity of GBS to adhere to epithelial cells. Indeed, compared to wild type strain 2603 pAM401*bibA* strain showed an increased adherence to both ME180 and A549 cells (**FIGS. 23A** and **23B**).

[333] As previously shown in **FIG. 19**, we were able to express in the 515 Ia strain, which does not expose BibA on the surface, the 2603 V/R form of BibA (515 pAM401*bibA*). In order to demonstrate that such expression was associated to a functional adhesive phenotype as for 2603 V/R wild type strain, we compared association levels to epithelial cells between 515 Ia wild type strain and 515 pAM401*bibA*. We observed that BibA exposure on 515 Ia surface resulted in a significant increase in the percentage of associated bacteria to both ME180 and A549 cells (**FIGS. 23A** and **23B**). This phenotype was also evident by confocal microscopy imaging (**FIGS. 23E** and **23F**).

EXAMPLE 20

BibA genomic characterization

[334] Genomic analysis on the recently sequenced genomes of 2603 V/R (Tettelin *et al.*, 2002), NEM316 type III (Glaser *et al.*, 2002), COH1 type III, CJB111 type V, 515 type Ia, 18RS21 type II and A909 type Ia (Tettelin *et al.*, 2005) strains shows that *bibA* is present in all these strains, although interrupted by the insertion of two putative transposases on the opposite strand in A909. This insertion causes the interruption of the reading frame at nucleotide 580. The *bibA* gene present on 515 Ia strain shows a frame-shift, which results in a truncated form of the protein (**FIG. 19G**), consisting of the N-terminal 376 amino acids and lacking the proline-rich and cell wall anchoring regions. A similar frame-shift occurs in CJB111 strain, resulting in the translation of the N-terminal 469 amino acids. Such a protein fragment was found in CJB111 supernatants. Western blot analysis of GBS supernatants from 31 strains representing the most common serotypes, revealed that BibA was present in 81% of the strains (**Table 4**).

[335] On the other hand, FACS analysis showed that BibA was expressed on the surface of 58% of the strains, while in 19% of them BibA was exclusively recovered in bacterial supernatants. However, BibA exposure on bacterial surface totally correlated with the presence in the supernatant.

[336] In general, two different types of sequence variability can be observed among the different BibA proteins. The first is the presence of a variable number of brief amino acid modules, which can be observed either within the N-terminal domain, or within the proline-rich tract. In particular, the presence of a region of 97 amino acids, holding the repeats IKAESIN (SEQ ID NO:65) and KIQXKXNT (SEQ ID NO:66) is observed within the N-terminal domain in A909, CJB11 and H36B, while the number of copies of the PEAK/PDVK modules varies between 17 and 42 (see **Table 3**). This suggests the insertion/excision of transposable elements.

[337] The second source of sequence variation consists of a non-repetitive tract of 97 residues within proline-reach region, which characterizes 515, NEM316, H36B, CJB111 and A909 strains. Collectively, the sequence analysis reveals that the protein exists in three different variants, one formed by strains 2603, 18RS21, and COH1, the other by NEM316 and 515, and the last one originated by CJB111, H36B and A909 (**FIG. 24**). However, the multiple alignment of the BibA amino acid sequences, shows that the protein is generally well conserved (amino acid identity ranges between 63.3 and 100% among N-terminal domains of different strains), with the exception of COH1, whose N-terminal region shows on average about 25% of amino acid identity to the other alleles.

EXAMPLE 21

Active Maternal Immunization Assay

[338] A maternal immunization/neonatal pup challenge model of GBS infection is used to verify the protective efficacy of the antigens in mice. See Rodewald *et al.*, *J. Infect. Diseases* **166**, 635, 1992. CD-1 female mice (6-8 weeks old) are immunized before breeding. The mice receive 20 μg of protein per dose when immunized with a single antigen and 60 μg of protein per dose (15 μg of each antigen) when immunized with the combination of antigens. Mice are bred 2-7 days after the last immunization. Within 48 h of birth, pups are injected intraperitoneally with 50 μl of GBS culture. Challenge inocula are prepared starting from frozen cultures diluted to the appropriate concentration with

THB before use. In preliminary experiments, the challenge doses per pup for each strain tested is determined to cause 90% lethality. Survival of pups is monitored for 2 days after challenge. Protection is calculated as (percentage deadControl minus percentage deadVaccine) divided by percentage deadControl multiplied by 100. Data are evaluated for statistical significance by Fisher's exact test.

EXAMPLE 22

BibA knock-out mutant strain is cleared more easily in human blood

[339] The importance of BibA expression in bacterial survival *in vivo* was assessed in freshly drawn blood from human donors. GBS was grown up to OD_{600} 0.4, washed, and resuspended in PBS. Inocula of 10^4 CFU in 100 µl were mixed with 300 µl of freshly drawn human blood using heparin as anticoagulant. The tubes were incubated for 3 hours with agitation at 37 °C, and dilutions were plated for determination of CFU.

[340] As shown in Table 5, 2603 V/R wild-type strain and the isogenic 2603Δ*bibA* knock-out mutant strain were compared for the capacity to replicate in whole human blood. The bacterial survival index was calculated as the ratio between the number of bacteria recovered at the end of the assay versus bacteria at time 0. We tested five individual donors and found that 2603 V/R wild-type strain proliferated in human blood 5 times more efficiently than the 2603Δ*bibA* mutant strain. However, survival indexes varied among the different donors. In three donors, where the wild-type strain replicated slowly in blood (from 5 to 14 times), the *bibA* knock-out mutant strain was almost cleared. By contrast, in two donors where the wild-type strain replicated highly in blood (77 and 41 times), the *bibA* mutant strain still proliferated, although less efficiently (37 and 5 times, respectively). These findings suggest that in donors with a reduced anti-bactericidal activity, the contribution of BibA to GBS survival in blood is less pronounced.

EXAMPLE 23

Complement-mediated GBS killing by Polymorphonuclear leukocytes (PMNs) is affected by BibA expression

[341] Phagocytic clearance of GBS by human blood is mainly mediated by PMNs which kill opsonized bacteria in the presence of complement. The killing by human PMNs of the 2603 V/R wild-type strain and the *bibA* mutant strains were compared. PMNs were obtained from heparin-anticoagulated venous blood of normal, healthy volunteers by dextran sedimentation, Ficoll-Hypaque density gradient centrifugation, and hypotonic lysis of residual erythrocytes, as described in Maione *et al.*, *Science 309*, 148-50.

[342] To prepare bacteria for killing experiments, 2603 V/R and 2603Δ*bibA* grown in THB medium were collected in mid-log pase of growth (OD_{600} 0.4), washed in HBSS (Gibco-BRL), and adjusted to a density of 10^7 CFU/ml. GBS (10^6 CFU) were opsonized for 15 minutes at 37 °C with 5% human serum containing anti-GBS antibodies. The bacteria were incubated for 3 h with PMNs and the number of surviving bacteria was determined by quantitative plating on TSA plates.

[343] Incubation of GBS with human serum alone resulted in no killing. As shown in **FIG. 30**, at the end of the 3 h incubation, the *bibA* mutant strain was killed more efficiently than the wild-type strain. Indeed, only 7% of the mutant bacteria survived phagocytosis by PMNs, compared to 30% for the wild-type strain. Heat inactivation of complement resulted in survival of both wild-type and *bibA* mutant strains, which replicated 5- to 6-fold during the time span of the experiment (**FIG. 30**).

Table 1.

	Total h-IgG	h-IgG1 (λ)	h-IgG2 (κ)	hIgG3 (κ)	Bovine IgG	Human serum IgG	Mouse serum IgG	Rabbit serum IgG
BibA-His	+++	-	-	-	-	+++	-	+
BibA-Nt-His	++	-	-	-	-	++	-	-
BibA-Ct-His	+	-	-	-	-	-	-	-

Table 2.

	Human serum IgA	Human colostrum-IgA
BibA-His	+++	+++
BibA-Nt-His	++	+
BibA-Ct-His	-	++

Table 3

GBS strain	Serotype	Surface*	Supernatant°	MW (kDa)
A909	Ia	-	-	-
515	Ia	-	+	38
DK1	Ia	+++	+	90
2177	Ib/c	-	+	90
5551	Ib/c	+++	+	80
H36B	Ib	++	+	90
2129	Ib	+	+	80
7357b	Ib	++	+	80
5518	Ib	-	-	-
18RS21	II	++	+	80
3050	II	+++	+	80
5401	II	-	+	70
2141	II	++	+	80
M732	III	-	-	-
M781	III	-	+	60
COH1	III	-	-	-
5435	III/R	-	+	60
5376	III/R	-	-	-
1998	III/R	+++	+	80
2274	IV	-	+	40
1999	IV	+	+	90
2210	IV	+	+	80
2603	V	+++	+	80
CJB111	V	-	+	48
5364	V	++	+	80
2110	V/c	++	+	80
2189	VIII	-	-	-
JM9130013	VIII	++	+	98
JMU071	VIII	++	+	98
CJB110	NT	+	+	60
1169	NT	++	+	60

*

(-) MFI 0-50
(+) MFI 50-100
(++) MFI 100-200
(+++) MFI 200-300

°

(-) WB negative
(+) WB positive

Table 4

GBS strain	PEAK/PDVK modules
COH1	17
NEM316	21
A909	25
CJB111	29
H36B	38
2603	42
515	42
18RS21	42

Table 5

Survival Index (% survival)	Donor A	Donor B	Donor C	Donor D	Donor E	% survival (mean ± SD)
2603 V/R	5.2 (100)	77.5 (100)	5.4 (100)	14.7 (100)	41.3 (100)	100
2603Δ*bibA*	0.7 (12.9)	37.6 (48.5)	0.76 (14.1)	1.3 (8.8)	5.4 (13.1)	19.5 ± 14.6

REFERENCES

Areschoug *et al.*, A proline-rich region with a highly periodic sequence in Streptococcal beta protein adopts the polyproline II structure and is exposed on the bacterial surface. *J Bacteriol* 184: 6376-6383 (2002).

Bae, T., and Schneewind, O. (2003) The YSIRK-G/S motif of staphylococcal protein A and its role in efficiency of signal peptide processing. *J Bacteriol* 185: 2910-2919.

Barreiro, C., Gonzalez-Lavado, E., and Martin, J.F. (2001) Organization and transcriptional analysis of a six-gene cluster around the rplK-rplA operon of Corynebacterium glutamicum encoding the ribosomal proteins L11 and L1. *Appl Environ Microbiol* 67: 2183-2190.

Beckmann, C., Waggoner, J.D., Harris, T.O., Tamura, G.S., and Rubens, C.E. (2002) Identification of novel adhesins from Group B streptococci by use of phage display reveals that C5a peptidase mediates fibronectin binding. *Infect Immun* 70: 2869-2876.

Berger, B., Wilson, D.B., Wolf, E., Tonchev, T., Milla, M., and Kim, P.S. (1995) Predicting coiled coils by use of pairwise residue correlations. *Proc Natl Acad Sci U S A* 92: 8259-8263.

Berggard, K., Johnsson, E., Morfeldt, E., Persson, J., Stalhammar-Carlemalm, M., and Lindahl, G. (2001) Binding of human C4BP to the hypervariable region of M protein: a molecular mechanism of phagocytosis resistance in Streptococcus pyogenes. *Mol Microbiol* 42: 539-551.

Bevanger, L. (1983) Ibc proteins as serotype markers of group B streptococci. *Acta Pathol Microbiol Immunol Scand [B]* 91: 231-234.

Blom, A.M., Villoutreix, B.O., and Dahlback, B. (2004) Complement inhibitor C4b-binding protein-friend or foe in the innate immune system? *Mol Immunol* 40: 1333-1346.

Boyle, M.D.P. (1998) Bacterial immunoglobulin-binding proteins. In *Encyclopedia of immunology*. New York: Academic Press, Inc., pp. 323-327.

Carlsson, F., Berggard, K., Stalhammar-Carlemalm, M., and Lindahl, G. (2003) Evasion of phagocytosis through cooperation between two ligand-binding regions in Streptococcus pyogenes M protein. *J Exp Med* 198: 1057-1068.

Carlsson, F., Sandin, C., and Lindahl, G. (2005) Human fibrinogen bound to Streptococcus pyogenes M protein inhibits complement deposition via the classical pathway. *Mol Microbiol* 56: 28-39.

Cheng, Q., Stafslien, D., Purushothaman, S.S., and Cleary, P. (2002) The group B streptococcal C5a peptidase is both a specific protease and an invasin. *Infect Immun* 70: 2408-2413.

Courtney, H.S., Bronze, M.S., Dale, J.B., and Hasty, D.L. (1994) Analysis of the role of M24 protein in group A streptococcal adhesion and colonization by use of omega-interposon mutagenesis. *Infect Immun* 62: 4868-4873.

Courtney, H.S., Ofek, I., and Hasty, D.L. (1997) M protein mediated adhesion of M type 24 Streptococcus pyogenes stimulates release of interleukin-6 by HEp-2 tissue culture cells. *FEMS Microbiol Lett* 151: 65-70.

Cunningham, M.W. (2000) Pathogenesis of group A streptococcal infections. *Clin Microbiol Rev* 13: 470-511.

Dave, S., Carmicle, S., Hammerschmidt, S., Pangburn, M.K., and McDaniel, L.S. (2004) Dual roles of PspC, a surface protein of Streptococcus pneumoniae, in binding human secretory IgA and factor H. *J Immunol* 173: 471-477.

Downing, W.L., Sullivan, S.L., Gottesman, M.E., and Dennis, P.P. (1990) Sequence and transcriptional pattern of the essential Escherichia coli secE-nusG operon. *J Bacteriol* 172: 1621-1627.

Fagan, P.K., Reinscheid, D., Gottschalk, B., and Chhatwal, G.S. (2001) Identification and characterization of a novel secreted immunoglobulin binding protein from group A streptococcus. *Infect Immun* 69: 4851-4857.

Fuller, T.E., Shea, R.J., Thacker, B.J., and Mulks, M.H. (1999) Identification of in vivo induced genes in Actinobacillus pleuropneumoniae. *Microb Pathog* 27: 311-327.

Glaser, P., Rusniok, C., Buchrieser, C., Chevalier, F., Frangeul, L., Msadek, T., Zouine, M., Couve, E., Lalioui, L., Poyart, C., Trieu-Cuot, P., and Kunst, F. (2002) Genome sequence of Streptococcus agalactiae, a pathogen causing invasive neonatal disease. *Mol Microbiol* 45: 1499-1513.

Grifantini, R., Bartolini, E., Muzzi, A., Draghi, M., Frigimelica, E., Berger, J., Ratti, G., Petracca, R., Galli, G., Agnusdei, M., Giuliani, M.M., Santini, L., Brunelli, B., Tettelin, H., Rappuoli, R., Randazzo, F., and Grandi, G. (2002) Previously unrecognized vaccine candidates against group B meningococcus identified by DNA microarrays. *Nat Biotechnol* 20: 914-921.

Hery-Arnaud, G., Bruant, G., Lanotte, P., Brun, S., Rosenau, A., van der Mee-Marquet, N., Quentin, R., and Mereghetti, L. (2005) Acquisition of insertion sequences and the GBSi1 intron by Streptococcus agalactiae isolates correlates with the evolution of the species. *J Bacteriol* 187: 6248-6252.

Hollingshead, S.K., Fischetti, V.A., and Scott, J.R. (1986) Complete nucleotide sequence of type 6 M protein of the group A Streptococcus. Repetitive structure and membrane anchor. *J Biol Chem* 261: 1677-1686.

Horstmann, R.D., Sievertsen, H.J., Knobloch, J., and Fischetti, V.A. (1988) Antiphagocytic activity of streptococcal M protein: selective binding of complement control protein factor H. *Proc Natl Acad Sci U S A* 85: 1657-1661.

Janulczyk, R., Iannelli, F., Sjoholm, A.G., Pozzi, G., and Bjorck, L. (2000) Hic, a novel surface protein of Streptococcus pneumoniae that interferes with complement function. *J Biol Chem* 275: 37257-37263.

Jarva, H., Janulczyk, R., Hellwage, J., Zipfel, P.F., Bjorck, L., and Meri, S. (2002) Streptococcus pneumoniae evades complement attack and opsonophagocytosis by expressing the pspC locus-encoded Hic protein that binds to short consensus repeats 8-11 of factor H. *J Immunol* 168: 1886-1894.

Jarva, H., Jokiranta, T.S., Wurzner, R., and Meri, S. (2003) Complement resistance mechanisms of streptococci. *Mol Immunol* 40: 95-107.

Jarva, H., Hellwage, J., Jokiranta, T.S., Lehtinen, M.J., Zipfel, P.F., and Meri, S. (2004) The group B streptococcal beta and pneumococcal Hic proteins are structurally related immune evasion molecules that bind the complement inhibitor factor H in an analogous fashion. *J Immunol* 172: 3111-3118.

Jeong, S.M., Yoshikawa, H., and Takahashi, H. (1993) Isolation and characterization of the secE homologue gene of Bacillus subtilis. *Mol Microbiol* 10: 133-142.

Jerlstrom, P.G., Chhatwal, G.S., and Timmis, K.N. (1991) The IgA-binding beta antigen of the c protein complex of Group B streptococci: sequence determination of its gene and detection of two binding regions. *Mol Microbiol* 5: 843-849.

Johnson, D.R., and Ferrieri, P. (1984) Group B streptococcal Ibc protein antigen: distribution of two determinants in wild-type strains of common serotypes. *J Clin Microbiol* 19: 506-510.

Katayama, M., Sakai, Y., Okamoto, S., Ihara, F., Nihira, T., and Yamada, Y. (1996) Gene organization in the ada-rplL region of Streptomyces virginiae. *Gene* 171: 135-136.

Lauer, P., Rinaudo, C.D., Soriani, M., Margarit, I., Maione, D., Rosini, R., Taddei, A.R., Mora, M., Rappuoli, R., Grandi, G., and Telford, J.L. (2005) Genome analysis reveals pili in Group B Streptococcus. *Science* 309: 105.

Lindahl, G., Akerstrom, B., Vaerman, J.P., and Stenberg, L. (1990) Characterization of an IgA receptor from group B streptococci: specificity for serum IgA. *Eur J Immunol* 20: 2241-2247.

Lindahl, G., Stalhammar-Carlemalm, M., and Areschoug, T. (2005) Surface proteins of Streptococcus agalactiae and related proteins in other bacterial pathogens. *Clin Microbiol Rev* 18: 102-127.

Maguin, E., Prevost, H., Ehrlich, S.D., and Gruss, A. (1996) Efficient insertional mutagenesis in lactococci and other gram-positive bacteria. *J Bacteriol* 178: 931-935.

Miyake, K., Onaka, H., Horinouchi, S., and Beppu, T. (1994) Organization and nucleotide sequence of the secE-nusG region of Streptomyces griseus. *Biochim Biophys Acta* 1217: 97-100.

Pandiripally, V., Gregory, E., and Cue, D. (2002) Acquisition of regulators of complement activation by Streptococcus pyogenes serotype M1. *Infect Immun* 70: 6206-6214.

Pandiripally, V., Wei, L., Skerka, C., Zipfel, P.F., and Cue, D. (2003) Recruitment of complement factor H-like protein 1 promotes intracellular invasion by group A streptococci. *Infect Immun* 71: 7119-7128.

Perez-Caballero, D., Garcia-Laorden, I., Cortes, G., Wessels, M.R., de Cordoba, S.R., and Alberti, S. (2004) Interaction between complement regulators and Streptococcus pyogenes: binding of C4b-binding protein and factor H/factor H-like protein 1 to M18 strains involves two different cell surface molecules. *J Immunol* 173: 6899-6904.

Phillips, G.N., Jr., Flicker, P.F., Cohen, C., Manjula, B.N., and Fischetti, V.A. (1981) Streptococcal M protein: alpha-helical coiled-coil structure and arrangement on the cell surface. *Proc Natl Acad Sci U S A* 78: 4689-4693.

Podbielski, A., Hawlitzky, J., Pack, T.D., Flosdorff, A., and Boyle, M.D. (1994) A group A streptococcal Enn protein potentially resulting from intergenomic recombination exhibits atypical immunoglobulin-binding characteristics. *Mol Microbiol* 12: 725-736.

Poplawski, A., Gullbrand, B., and Bernander, R. (2000) The ftsZ gene of Haloferax mediterranei: sequence, conserved gene order, and visualization of the FtsZ ring. *Gene* 242: 357-367.

Puttikhunt, C., Nihira, T., and Yamada, Y. (1995) Cloning, nucleotide sequence, and transcriptional analysis of the nusG gene of Streptomyces coelicolor A3(2), which encodes a putative transcriptional antiterminator. *Mol Gen Genet* 247: 118-122.

Rost, B., and Sander, C. (1993) Prediction of protein secondary structure at better than 70% accuracy. *J Mol Biol* 232: 584-599.

Russell-Jones, G.J., Gotschlich, E.C., and Blake, M.S. (1984) A surface receptor specific for human IgA on group B streptococci possessing the Ibc protein antigen. *J Exp Med* 160: 1467-1475.

Sharp, P.M. (1994) Identification of genes encoding ribosomal protein L33 from Bacillus licheniformis, Thermus thermophilus and Thermotoga maritima. *Gene* 139: 135-136.

Song, X.M., Perez-Casal, J., Fontaine, M.C., and Potter, A.A. (2002) Bovine immunoglobulin A (IgA)-binding activities of the surface-expressed Mig protein of Streptococcus dysgalactiae. *Microbiology* 148: 2055-2064.

Stenberg, L., O'Toole, P., and Lindahl, G. (1992) Many group A streptococcal strains express two different immunoglobulin-binding proteins, encoded by closely linked genes: characterization of the proteins expressed by four strains of different M-type. *Mol Microbiol* 6: 1185-1194.

Syvanen, A.C., Amiri, H., Jamal, A., Andersson, S.G., and Kurland, C.G. (1996) A chimeric disposition of the elongation factor genes in Rickettsia prowazekii. *J Bacteriol* 178: 6192-6199.

Talay, S.R. (2005) Gram-positive adhesins. *Contrib Microbiol* 12: 90-113.

Tamura, G.S., Herndon, M., Przekwas, J., Rubens, C.E., Ferrieri, P., and Hillier, S.L. (2000) Analysis of restriction fragment length polymorphisms of the insertion sequence IS1381 in group B Streptococci. *J Infect Dis* 181: 364-368.

Tettelin *et al.*, Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae. *Proc Natl Acad Sci U S A* 99: 12391-12396, 2002.

Tettelin *et al.*, Genome analysis of multiple pathogenic isolates of Streptococcus agalactiae: Implications for the microbial "pan-genome". *Proc Natl Acad Sci U S A* 102: 13950-13955, 2005.

Thern, A., Stenberg, L., Dahlback, B., and Lindahl, G. (1995) Ig-binding surface proteins of Streptococcus pyogenes also bind human C4b-binding protein (C4BP), a regulatory component of the complement system. *J Immunol* 154: 375-386.

Thompson, J.D., Higgins, D.G., and Gibson, T.J. (1994) CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res* 22: 4673-4680.

Wang, J.R., and Stinson, M.W. (1994) M protein mediates streptococcal adhesion to HEp-2 cells. *Infect Immun* 62: 442-448.

Wexler, D.E., Chenoweth, D.E., and Cleary, P.P. (1985) Mechanism of action of the group A streptococcal C5a inactivator. *Proc Natl Acad Sci U S A* 82: 8144-8148.

CLAIMS

1. A BibA polypeptide comprising a portion of a BibA protein which portion is selected from the group consisting of:

(1) a coiled-coil domain of the BibA protein;

(2) a leader sequence and the coiled coil domain of the BibA protein;

(3) a proline-rich domain of the BibA protein;

(4) the coiled-coil domain and the proline-rich domain of the BibA protein; and

(5) the leader sequence, the coiled-coil domain, and the proline-rich domain of the BibA protein;

wherein the portion of the BibA protein is free of other contiguous amino acid sequences of the BibA protein.

2. The BibA polypeptide of claim 1, wherein the amino acid sequence of the BibA protein is at least 95% identical to SEQ ID NO:1.

3. The BibA polypeptide of claim 1 wherein the amino acid sequence of the BibA protein is SEQ ID NO:1.

4. The BibA polypeptide of claim 1 wherein the amino acid sequence of the proline-rich domain is at least 95% identical to SEQ ID NO:5.

5. The BibA polypeptide of claim 1 wherein the amino acid sequence of the proline-rich domain is SEQ ID NO:5.

6. The BibA polypeptide of claim 1 wherein the amino acid sequence of the coiled-coil domain is at least 95% identical to SEQ ID NO:7.

7. The BibA polypeptide of claim 1 wherein the amino acid sequence of the coiled-coil domain is SEQ ID NO:7.

8. The BibA polypeptide of claim 1 wherein the amino acid sequence of the leader sequence is at least 95% identical to amino acids 1-36 of SEQ ID NO:1.

9. The BibA polypeptide of claim 1 wherein the amino acid sequence of the leader sequence is amino acids 1-36 of SEQ ID NO:1.

10. The BibA polypeptide of claim 1 wherein the portion consists of the coiled-coil domain.

11. The BibA polypeptide of claim 1 wherein the portion consists of the leader sequence and the coiled-coil domain.

12. The BibA polypeptide of claim 11 wherein the amino acid sequence of the portion is at least 95% identical to SEQ ID NO:6.

13. The BibA polypeptide of claim 11 wherein the amino acid sequence of the portion is SEQ ID NO:6.

14. The BibA polypeptide of claim 1 wherein the portion consists of the proline-rich domain.

15. The BibA polypeptide of claim 1 wherein the portion consists of the coiled-coil domain and the proline-rich domain.

16. The BibA polypeptide of claim 15 wherein the amino acid sequence of the portion is at least 95% identical to SEQ ID NO:4.

17. The BibA polypeptide of claim 15 wherein the amino acid sequence of the portion is SEQ ID NO:4.

18. The BibA polypeptide of claim 1 wherein the portion consists of the leader sequence, the coiled-coil domain, and the proline-rich domain.

19. The BibA polypeptide of claim 18 wherein the amino acid sequence of the portion is at least 95% identical to SEQ ID NO:8.

20. The BibA polypeptide of claim 18 wherein the amino acid sequence of the portion is SEQ ID NO:8.

21. A composition comprising:

the BibA polypeptide of any of claims 1-20; and

a pharmaceutically acceptable carrier.

22. The composition of claim 21, further comprising a second polypeptide.

23. The composition of claim 22, wherein said polypeptide is selected from the group consisting of GBS1-GBS689.

24. An isolated nucleic acid molecule which encodes the BibA polypeptide of any of claims 1-20.

25. The isolated nucleic acid molecule of claim 24 which comprises a nucleotide sequence obtained from SEQ ID NO:16.

26. A composition comprising:

the nucleic acid molecule of claim 24 or 25; and

a pharmaceutically acceptable carrier.

27. The composition of claim 26 further comprising a second nucleic acid molecule which encodes a second polypeptide.

28. The composition of claim 27 wherein the second polypeptide is selected from the group consisting of GBS1-GBS689.

29. The composition of any of claims 21-23 wherein at least one of the polypeptides is coupled to a carrier protein.

30. The composition of claim 29 wherein the carrier protein is selected from the group consisting of a bacterial toxin, a bacterial toxoid, a *N. meningitidis* outer membrane protein, a heat shock protein, a pertussis protein, *H. influenzae* protein D, a cytokine, a lymphokine, a hormone, a growth factor, *C. difficile* toxin A, *C. difficile* toxin B, and an iron-uptake protein.

31. The composition of any of claims 21-30 further comprising an active agent which is useful in a pediatric vaccine.

32. The composition of claim 31 wherein the active agent is selected from the group consisting of:

(a) a polypeptide antigen selected from the group consisting of *N. meningitidis*, *S. pneumoniae*, *Bordetella pertussis*, *Moraxella catarrhalis*, *Clostridium tetani*, *Chorinebacterim diphteriae*, respiratory syncytial virus, polio virus, measles virus, mumps virus, rubella virus, and rotavirus polypeptide antigens; and

(b) a nucleic acid molecule which encodes the polypeptide antigen.

33. The composition of any of claims 21-30 further comprising a second active agent which is useful in a vaccine for elderly or immunocompromised individuals.

34. The composition of claim 33 wherein the second active agent is selected from the group consisting of:

(a) a polypeptide antigen selected from the group consisting of *Enterococcus faecalis*, *Staphylococcus aureaus*, *Staphylococcus epidermis*, *Pseudomonas aeruginosa*, *Legionella pneumophila*, *Listeria monocytogenes*, influenza virus, and parainfluenza virus polypeptide antigens; and

(b) a nucleic acid molecule which encodes the polypeptide antigen.

35. A method of treating or preventing infection by *Streptococcus agalactiae* comprising administering to an individual in need thereof an effective amount of the composition of any of claims 21-34.

36. A kit comprising:

a container comprising the composition of any of claims 21-34; and

instructions for using the composition to treat or prevent infection by *Streptococcus agalactiae*.

37. A method of making a vaccine for the prevention or treatment of infection by *Streptococcus agalactiae* comprising combining:

(a) the BibA polypeptide of any of claims 1-20; and

(b) a pharmaceutically acceptable carrier.

38. The method of claim 33 wherein the polypeptide is made by a method comprising:

(a) culturing a host cell comprising an expression construct which encodes the BibA polypeptide; and

(b) recovering the BibA polypeptide.

39. A method of making a vaccine for treating or preventing infection by *Streptococcus agalactiae* comprising combining:

(a) the nucleic acid molecule of claim 24 or 25; and

(b) a pharmaceutically acceptable carrier.

40. Use of the BibA polypeptide of any of claims 1-20 in the manufacture of a medicament for treating or preventing infection by *Streptococcus agalactiae*.

41. Use of the nucleic acid molecule of claims 24 or 25 in the manufacture of a medicament for treating or preventing infection by *Streptococcus agalactiae*.

42. A preparation of antibodies which specifically bind to the BibA polypeptide of any of claims 1-20.

43. The preparation of claim 42 wherein the antibodies are polyclonal.

44. The preparation of claim 42 wherein the antibodies are monoclonal.

45. The preparation of claim 42 wherein the antibodies are selected from the group consisting of $F(ab')_2$ fragments, F(ab) fragments, F_v molecules, non-covalent heterodimers, single-chain Fv molecules, dimeric antibody fragment constructs, trimeric antibody fragment constructs, minibodies, diabodies, and chimeric antibodies.

46. The preparation of any of claims 42-45 wherein the antibodies are humanized.

47. The preparation of any of claims 42-45 wherein the antibodies are human antibodies.

48. The preparation of any of claims 42-47 wherein the antibodies specifically bind to an epitope in the coiled-coil domain of BibA.

49. The preparation of any of claims 42-47 wherein the antibodies specifically bind to an epitope in the N-terminal portion of BibA.

50. The preparation of any of claims 42-47 wherein the antibodies specifically bind to an epitope in the proline-rich domain of BibA.

51. A composition comprising:

the preparation of any of claims 42-50; and

a pharmaceutically acceptable carrier.

52. The composition of claim 51 further comprising an antibody which specifically binds to an active agent which is useful in a pediatric vaccine.

53. The composition of claim 52 wherein the active agent is a polypeptide antigen selected from the group consisting of *N. meningitidis*, *S. pneumoniae*, *Bordetella pertussis*, *Moraxella catarrhalis*, *Clostridium tetani, Chorinebacterim diphteriae*, respiratory syncytial virus, polio virus, measles virus, mumps virus, rubella virus, and rotavirus polypeptide antigens.

54. The composition of claim 51 further comprising an antibody which specifically binds to an active agent which is useful in a vaccine for elderly or immunocompromised individuals.

55. The composition of claim 54 wherein the active agent is a polypeptide antigen selected from the group consisting of *Enterococcus faecalis*, *Staphylococcus aureaus*, *Staphylococcus epidermis*, *Pseudomonas aeruginosa*, *Legionella pneumophila*, *Listeria monocytogenes*, influenza virus, and parainfluenza virus polypeptide antigens.

56. A method of treating or preventing *Streptococcus agalactiae* infection comprising administering to a patient in need thereof the composition of any of claims 51-55.

57. A kit comprising:

a container comprising a composition of claim 51; and

instructions for using the composition to treat or prevent infection by *S. agalactiae*.

58. A method of making a composition for treating or preventing infection by *Streptococcus agalactiae* comprising combining:

the preparation of any of claims 42-50; and

a pharmaceutically acceptable carrier.

59. Use of the preparation of any of claims 42-50 in the manufacture of a medicament for treating or preventing infection by *Streptococcus agalactiae*.

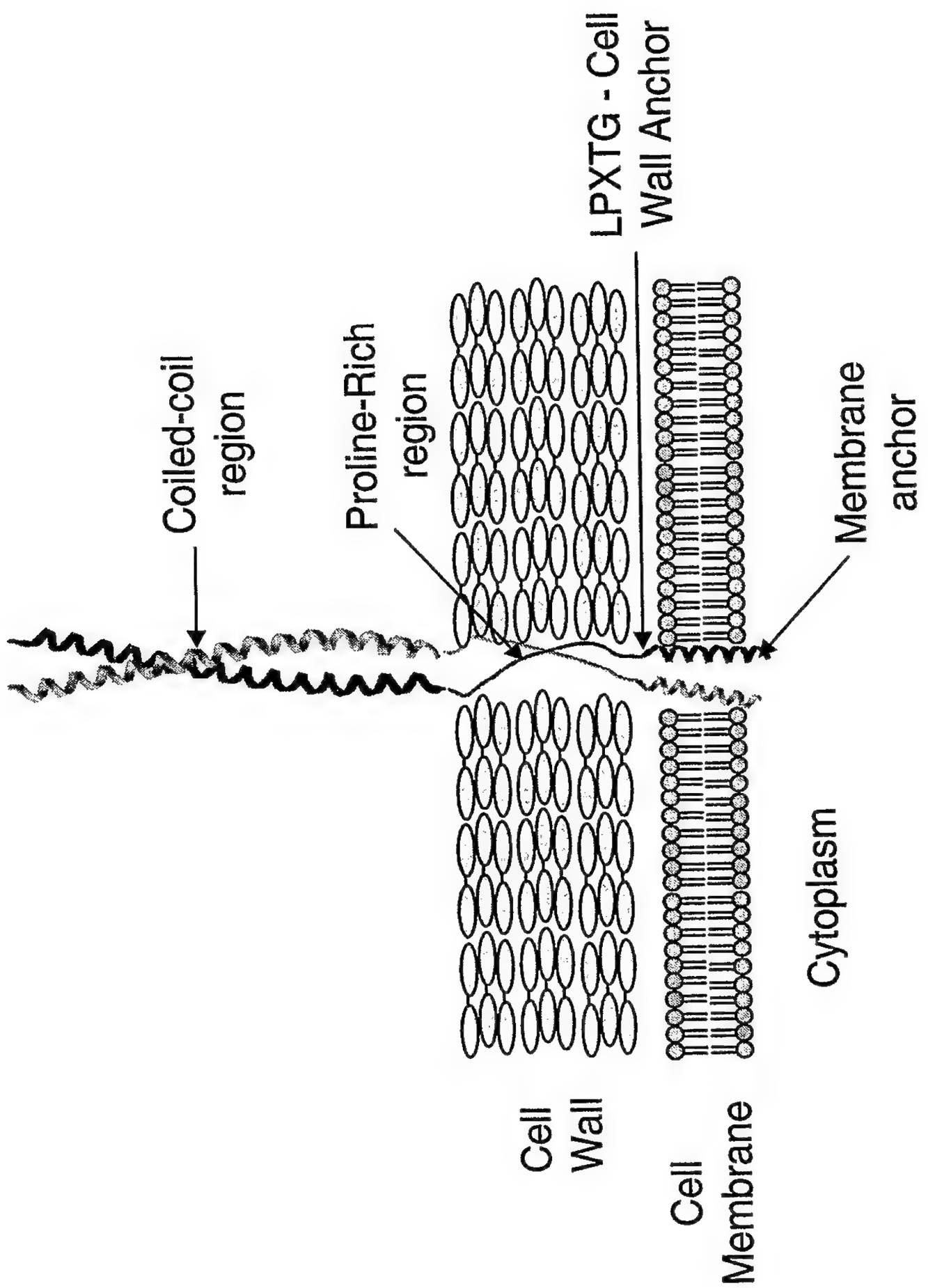
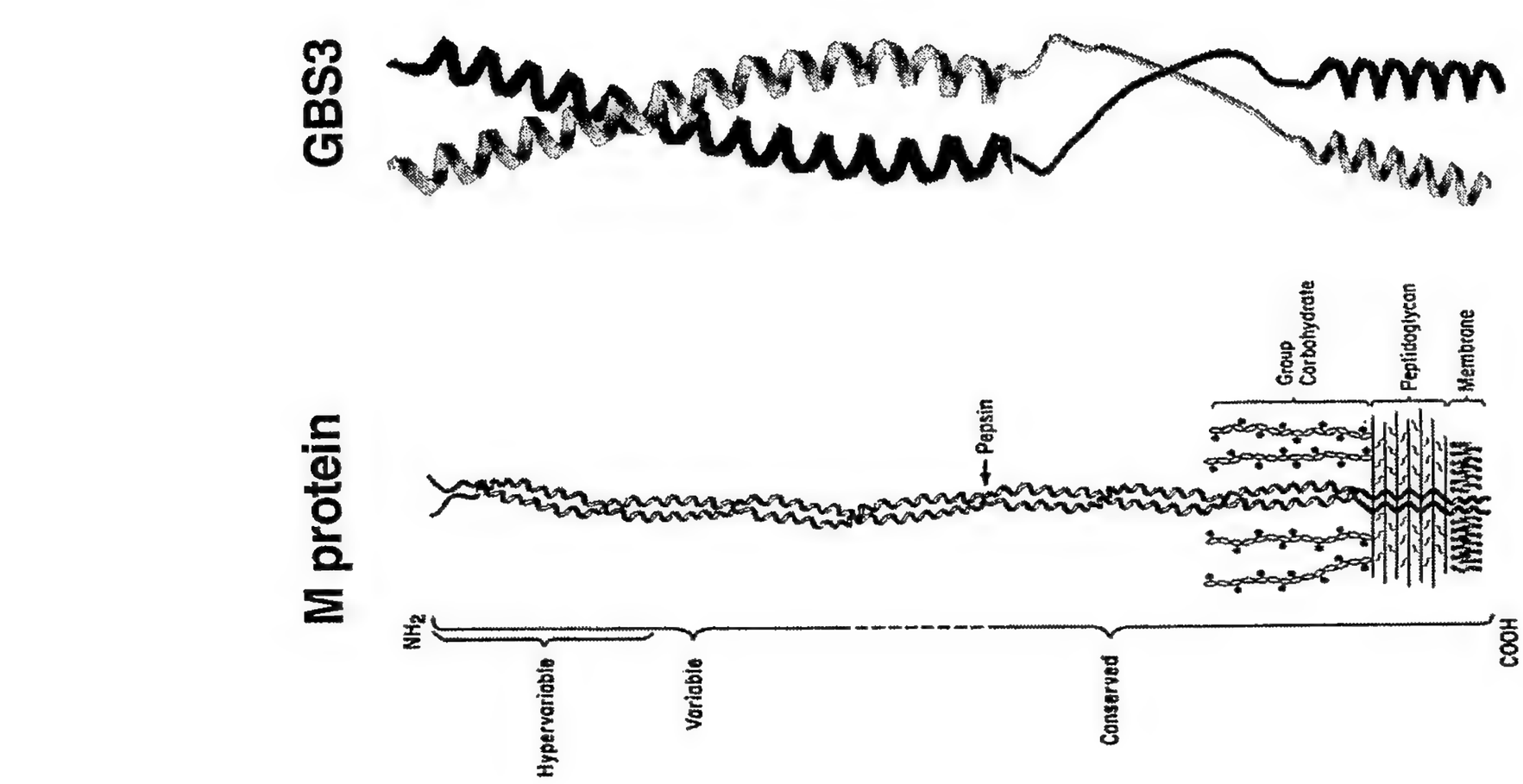

LPXTG - Cell Wall Anchor
Coiled-coil region
Proline-Rich region
Membrane anchor
Cytoplasm
Cell Wall
Cell Membrane

Fig. 1A

FIG. 1B


GBS3
M protein
Pepsin
Group Carbohydrate
Peptidoglycan
Membrane
NH2
COOH
Hypervariable
Variable
Conserved

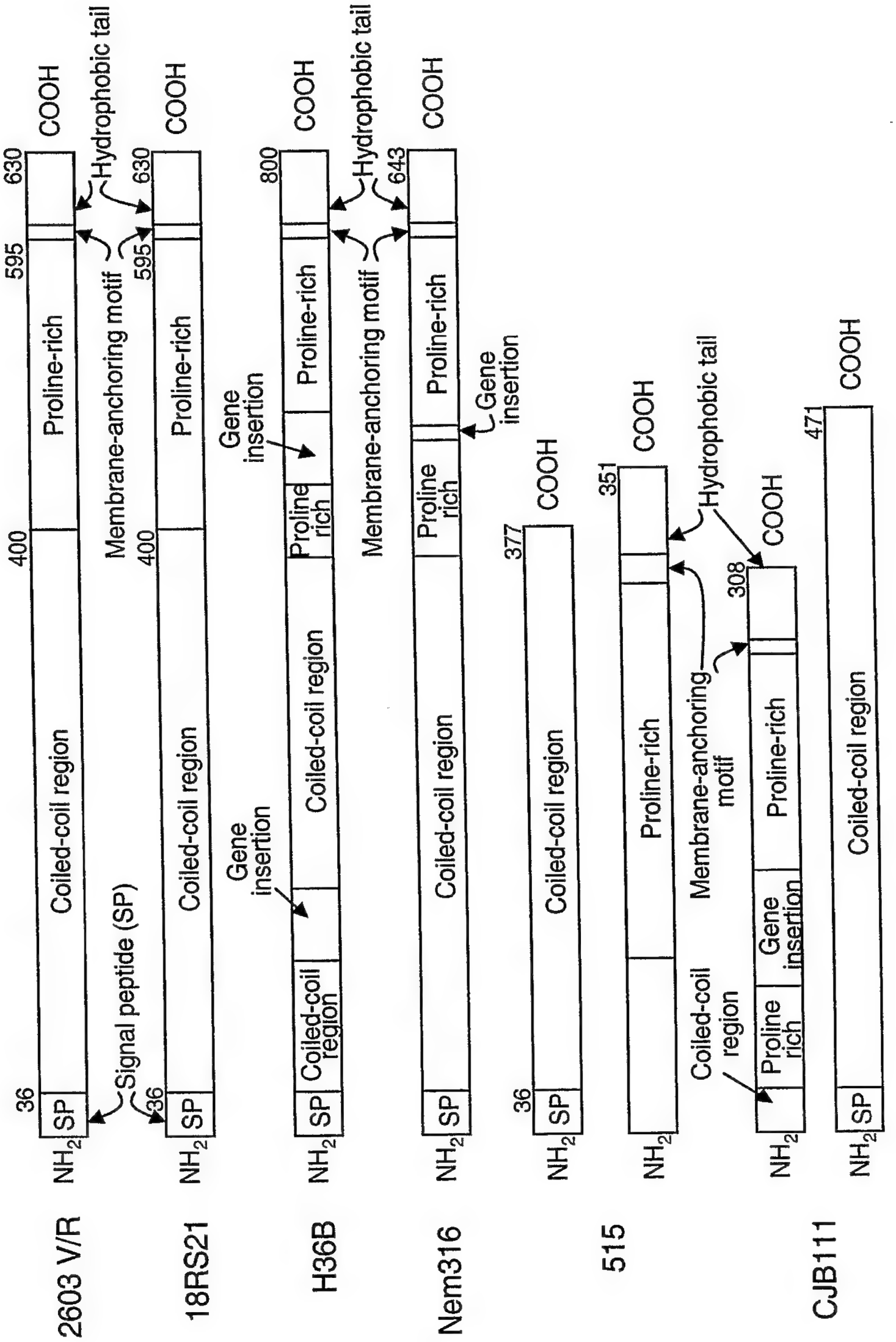
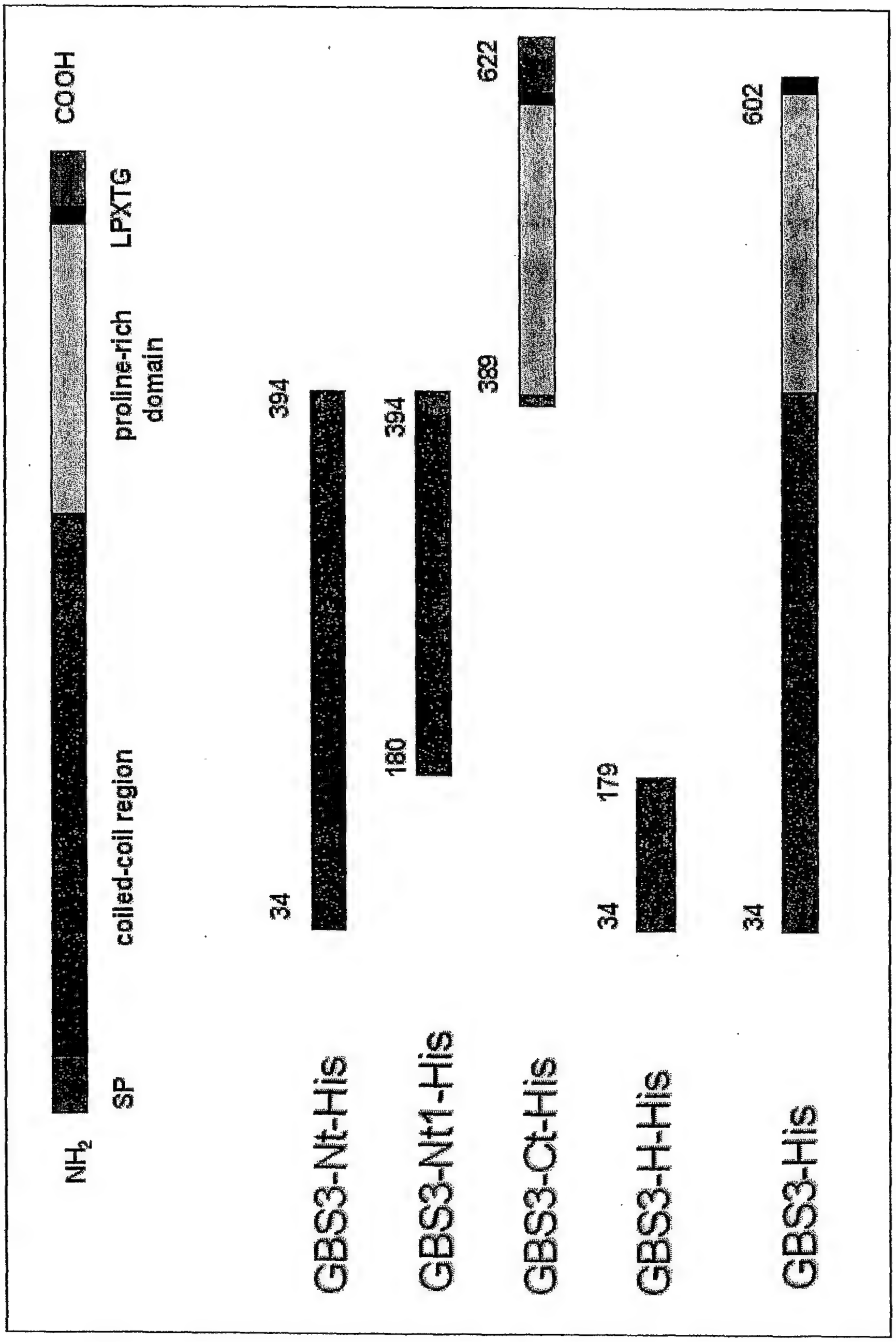

2603 V/R
18RS21
H36B
Nem316
515
CJB111
NH2
SP
36
Signal peptide (SP)
400
595
630
Coiled-coil region
Proline-rich
Membrane-anchoring motif
Hydrophobic tail
COOH
Gene insertion
Coiled-coil region
Proline rich
800
643
377
351
308
471
Proline-rich
Membrane-anchoring motif
Coiled-coil region

Fig. 2A

FIG. 2B


NH2
SP
COOH
LPXTG
proline-rich domain
coiled-coil region
34
394
180
394
389
622
34
179
34
602
GBS3-Nt-His
GBS3-Nt1-His
GBS3-Ct-His
GBS3-H-His
GBS3-His

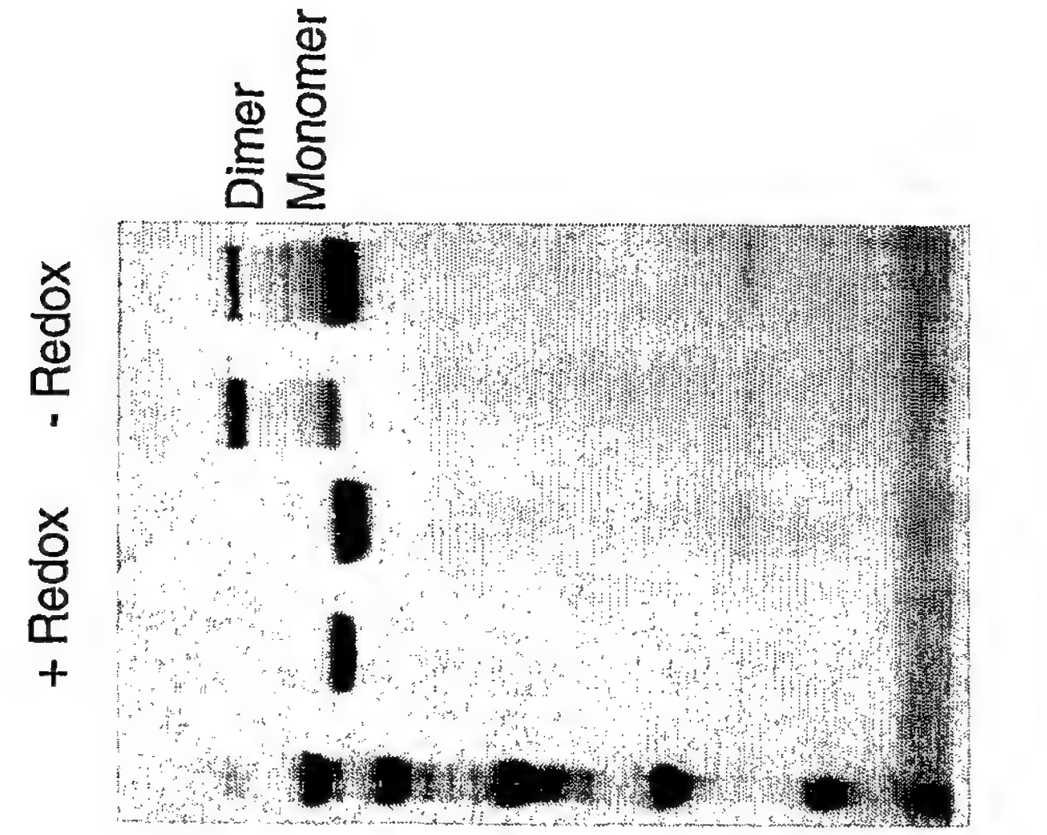


Fig. 3B

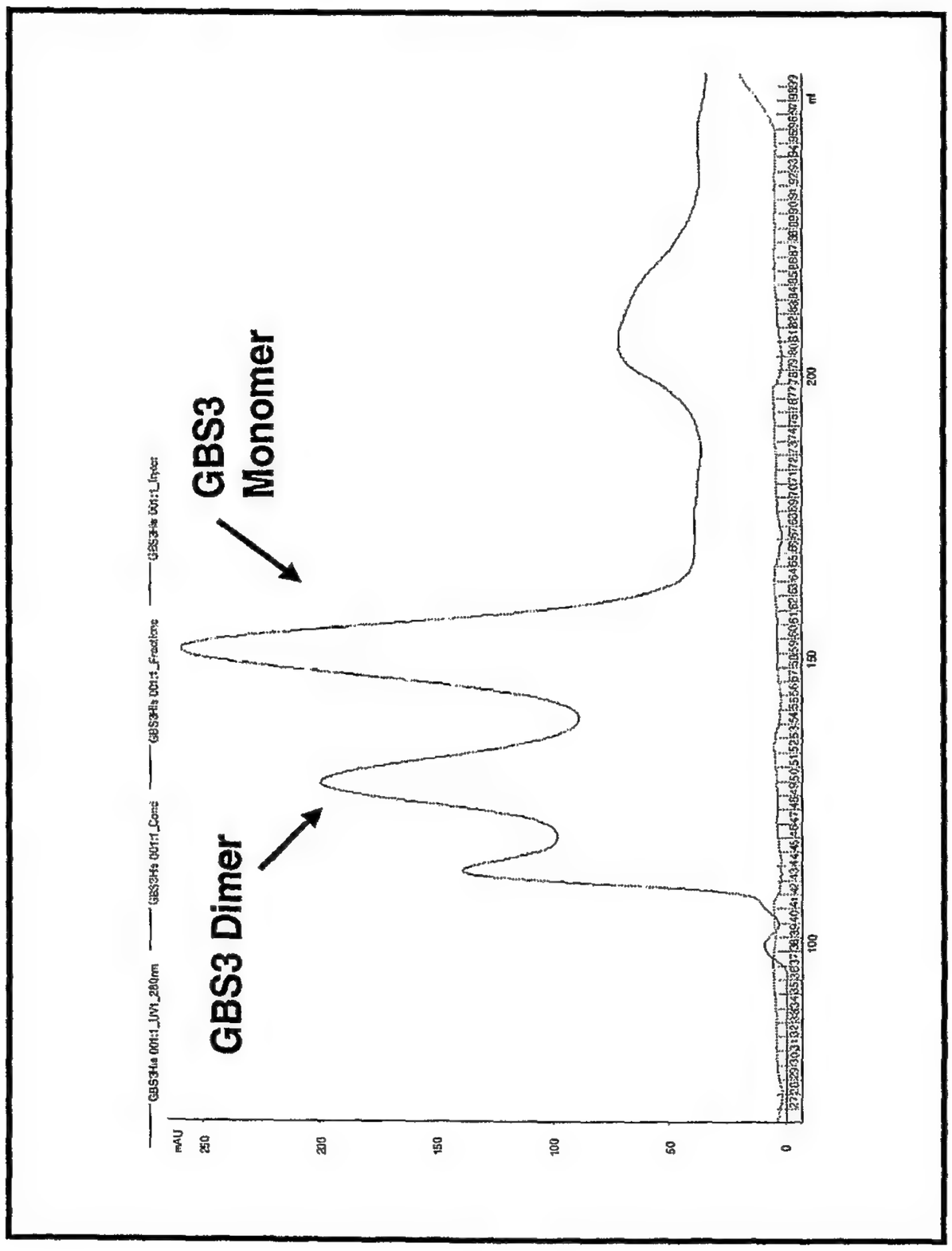


FIG. 3

Fig. 3A

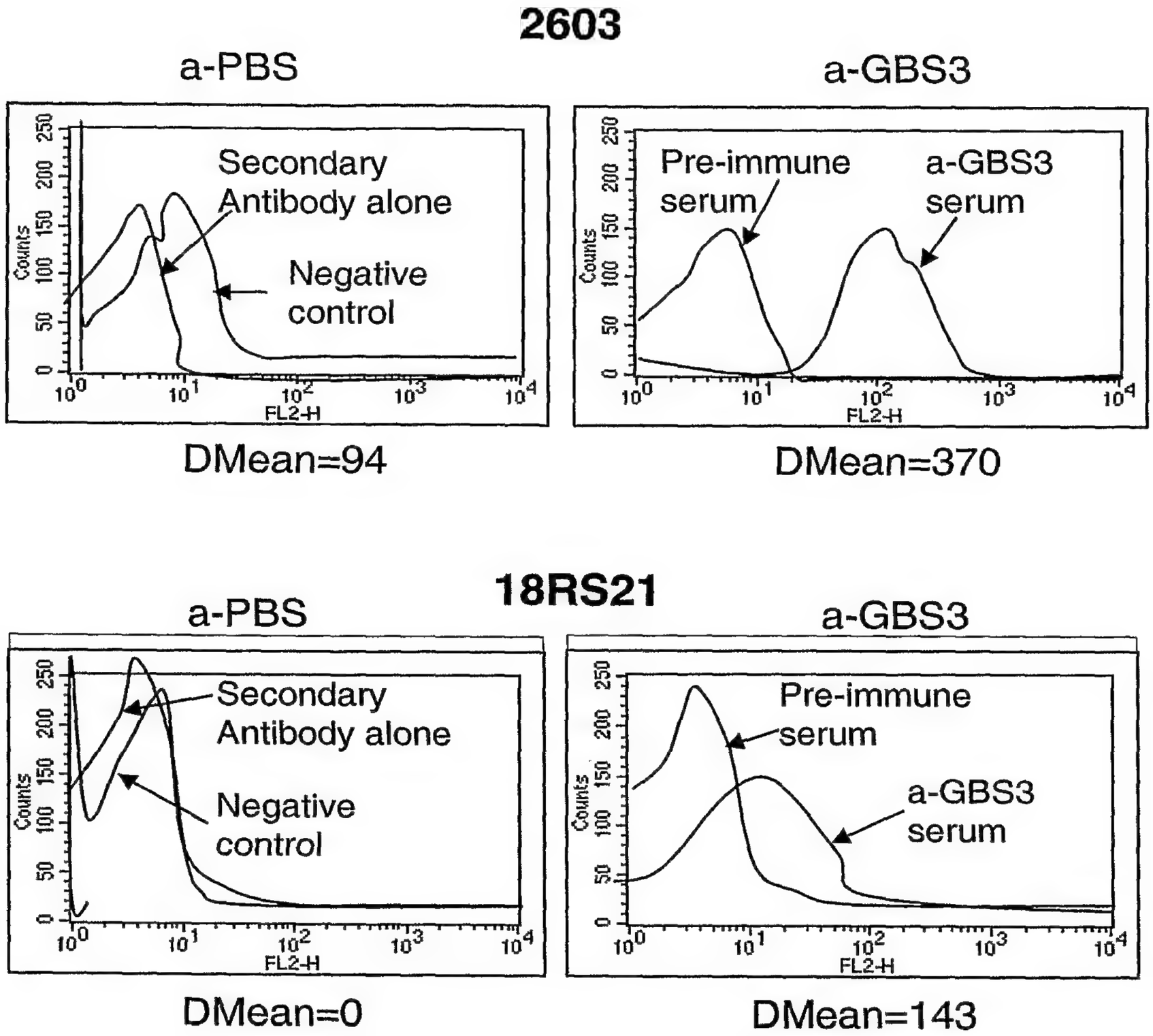

2603
a-PBS
a-GBS3
Secondary Antibody alone
Negative control
Pre-immune serum
a-GBS3 serum
Counts
FL2-H
DMean=94
DMean=370
18RS21
a-PBS
a-GBS3
Secondary Antibody alone
Negative control
Pre-immune serum
a-GBS3 serum
DMean=0
DMean=143
H36B
a-PBS
a-GBS3
Secondary Antibody alone
Negative control
Pre-immune serum
a-GBS3 serum
DMean=84
DMean=114

FIG. 4A

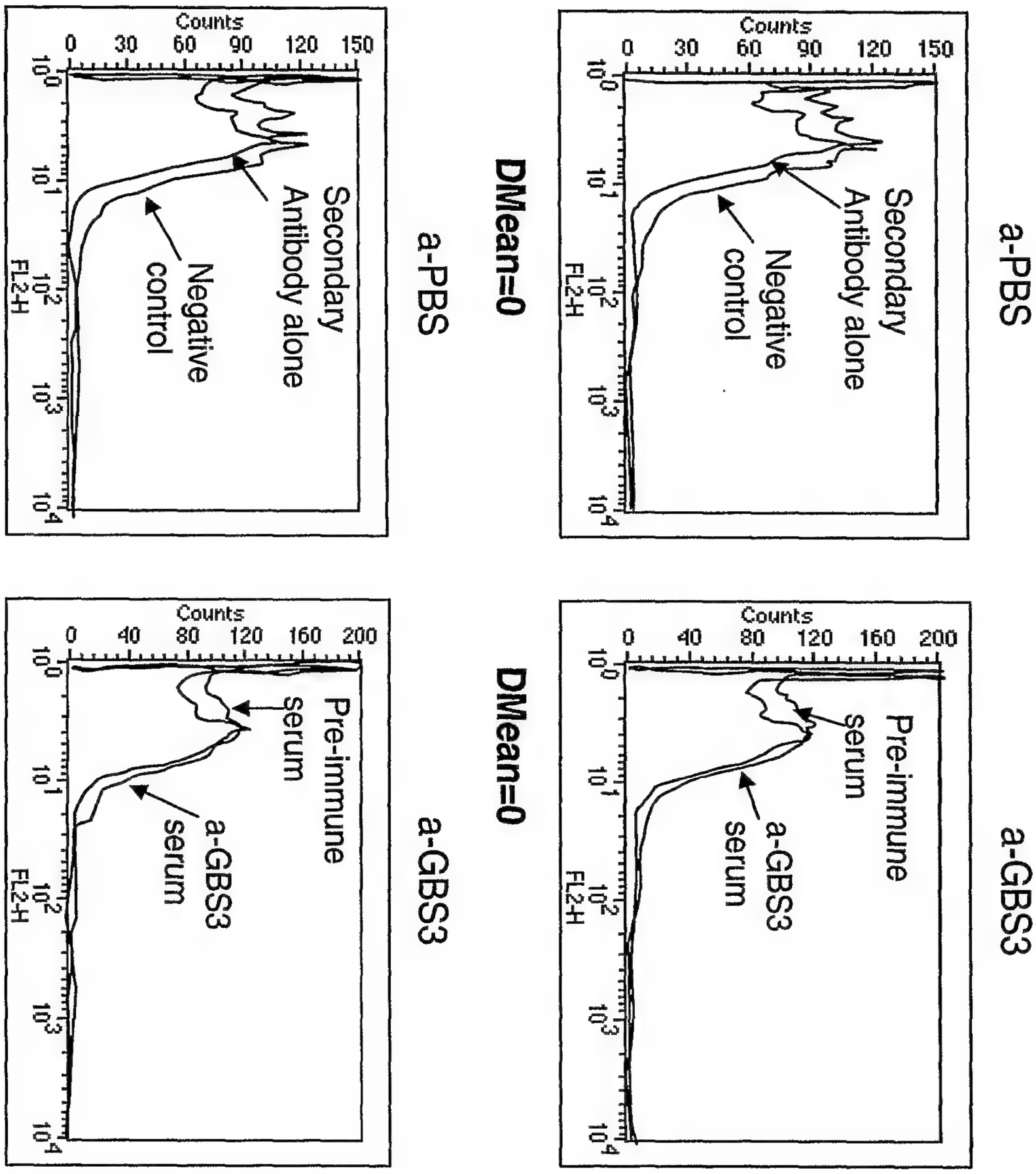
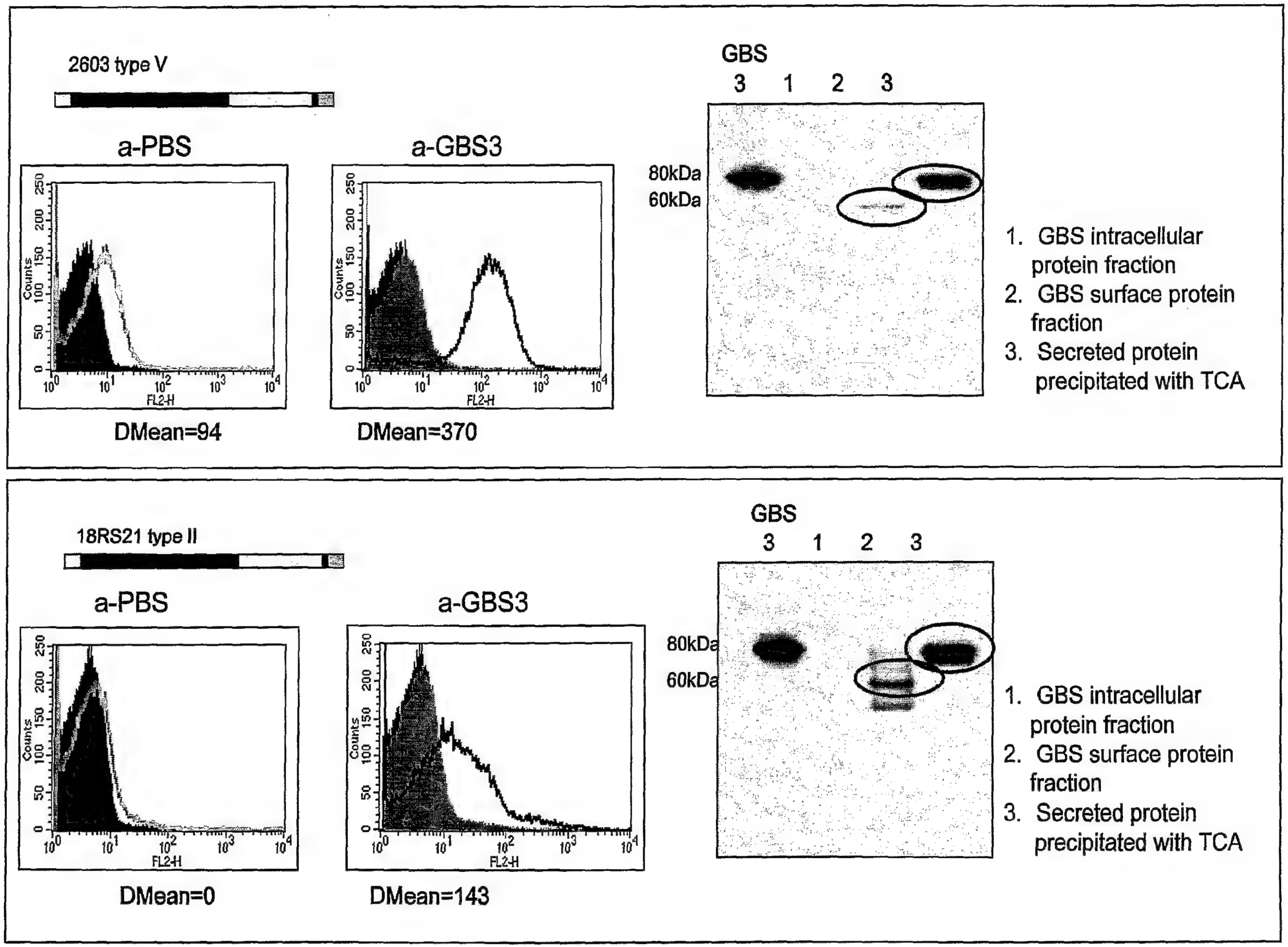

CJB111
515
a-PBS
a-GBS3
DMean=0
DMean=0
Counts
0 30 60 90 120 150
0 40 80 120 160 200
Secondary Antibody alone
Negative control
Pre-immune serum
a-GBS3 serum
FL2-H

Fig. 4B

FIG. 5A


2603 type V
a-PBS
a-GBS3
Counts
FL2-H
DMean=94
DMean=370
GBS
3 1 2 3
80kDa
60kDa
1. GBS intracellular protein fraction
2. GBS surface protein fraction
3. Secreted protein precipitated with TCA
18RS21 type II
a-PBS
a-GBS3
Counts
FL2-H
DMean=0
DMean=143
GBS
3 1 2 3
80kDa
60kDa
1. GBS intracellular protein fraction
2. GBS surface protein fraction
3. Secreted protein precipitated with TCA

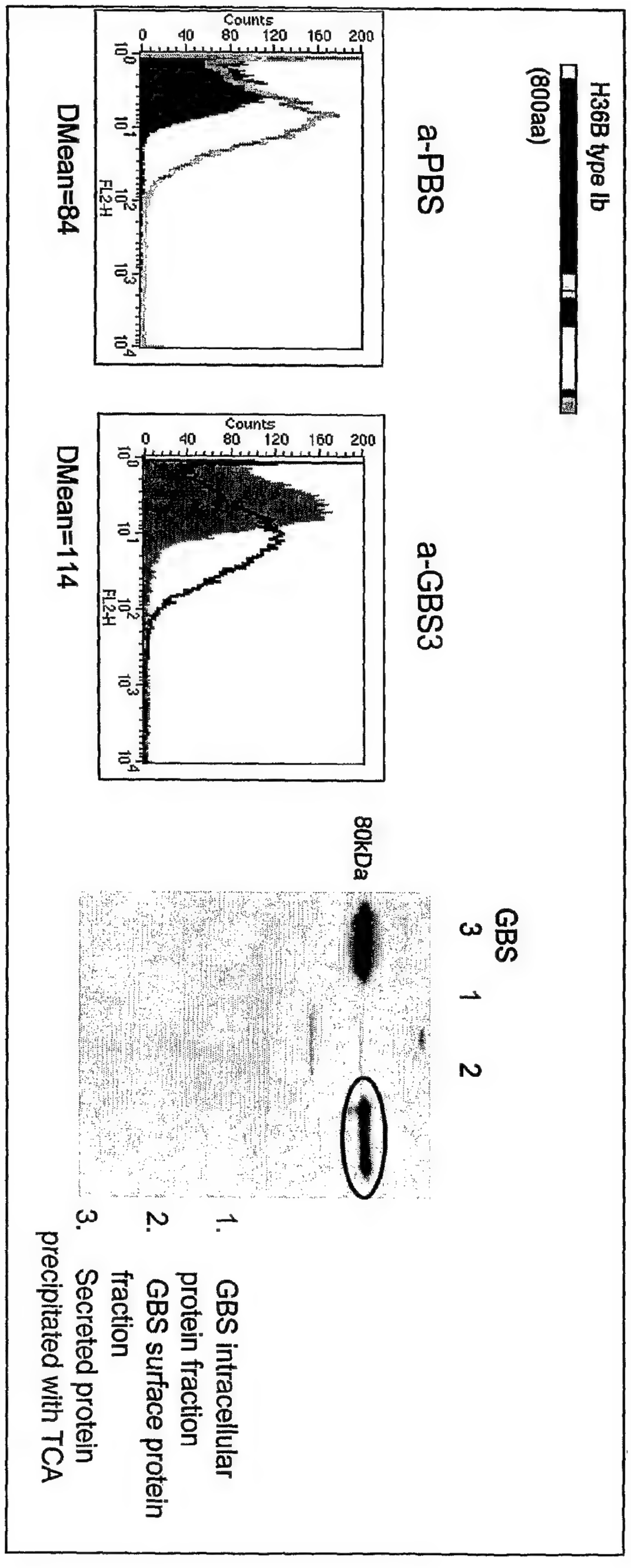
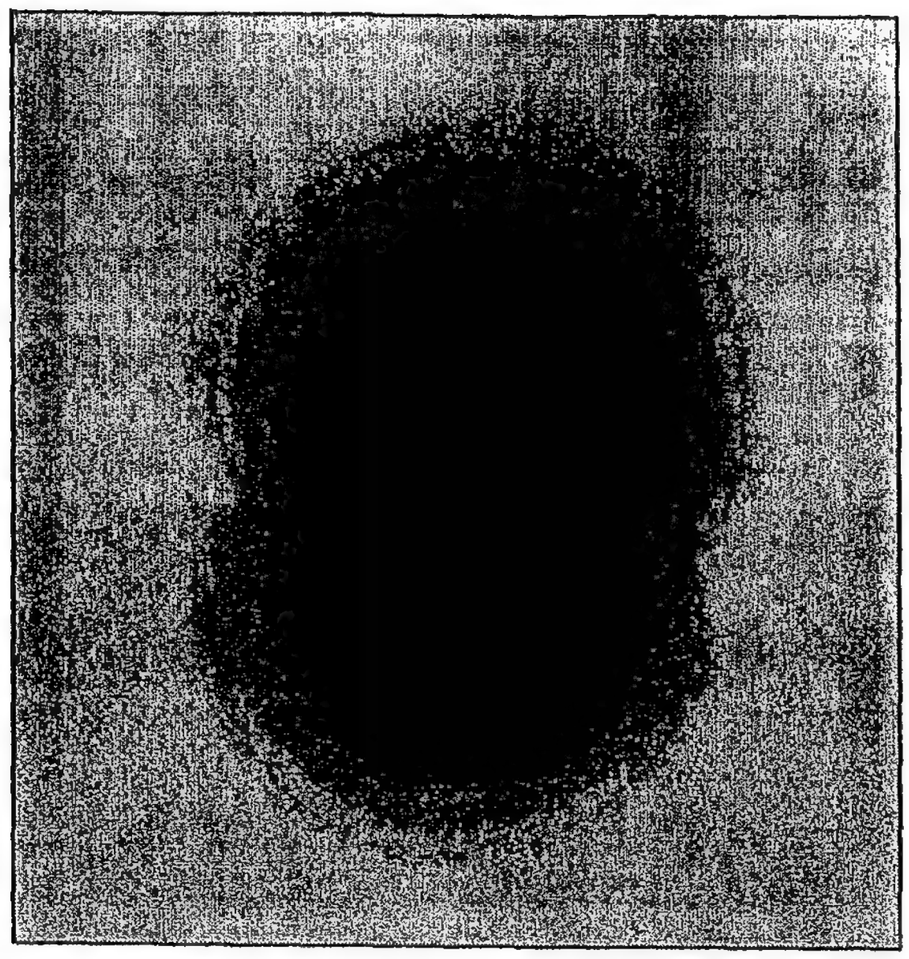

H36B type Ib
(800aa)
a-PBS
Counts
0 40 80 120 160 200
FL2-H
DMean=84
a-GBS3
DMean=114
GBS
3 1 2
80kDa
1. GBS intracellular protein fraction
2. GBS surface protein fraction
3. Secreted protein precipitated with TCA

FIG. 5B



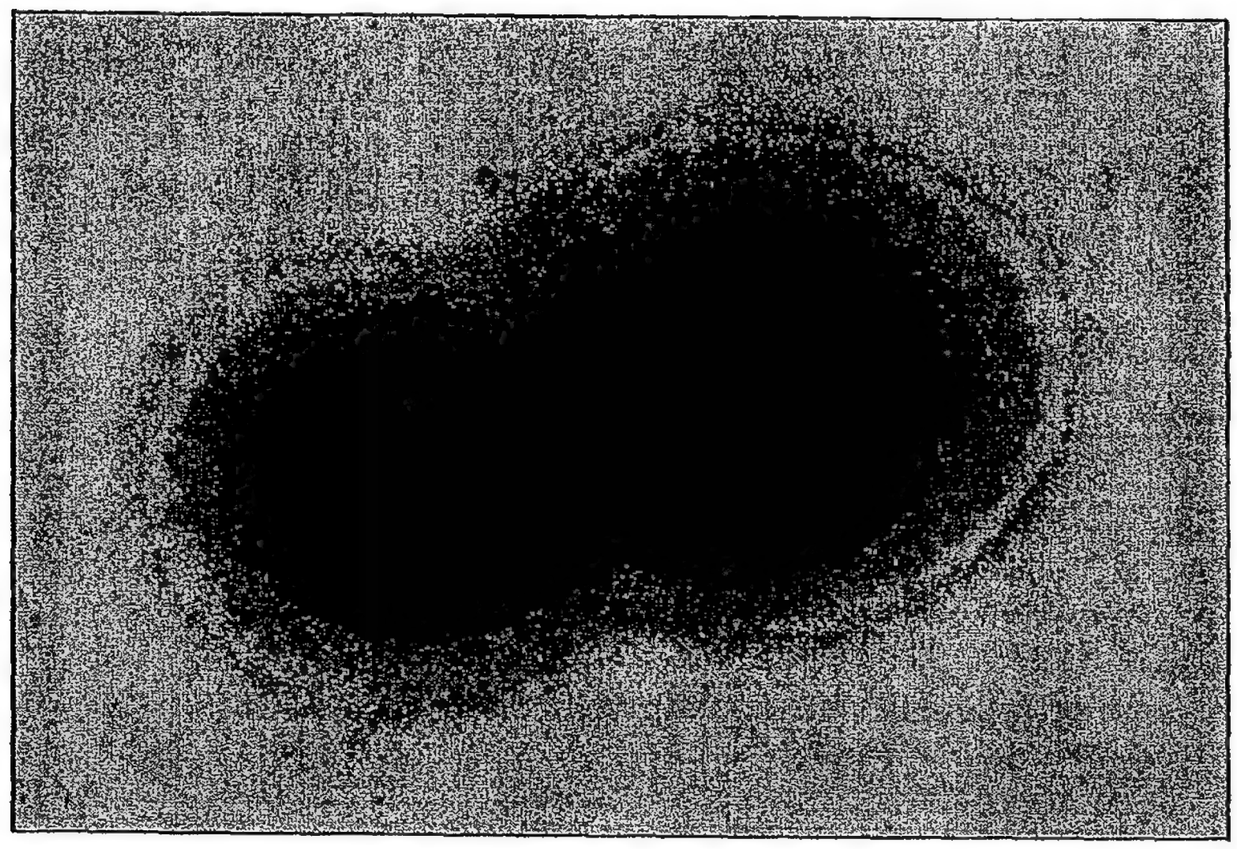


FIG. 6

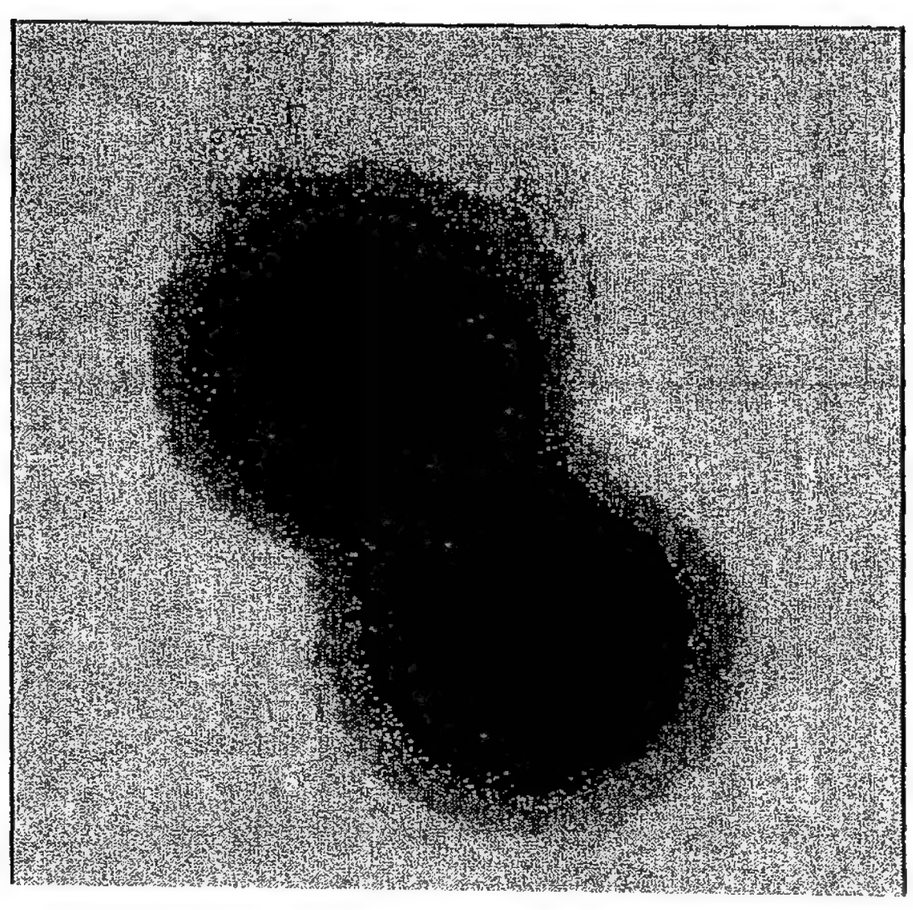
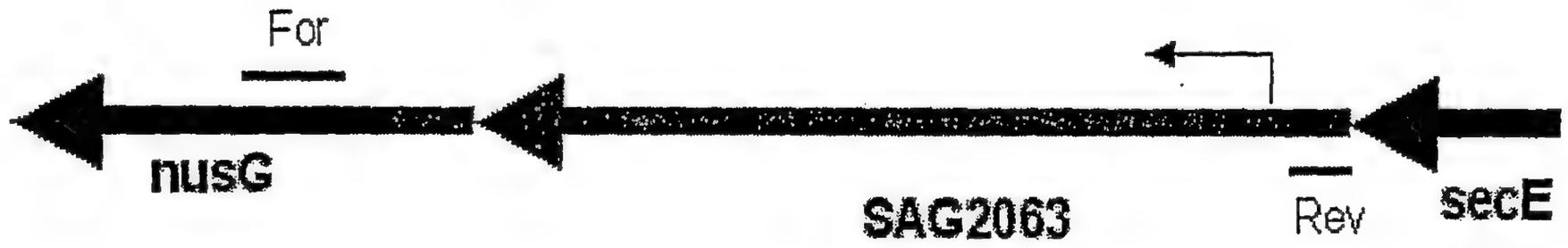


FIG.7A



GBS3 gene (SAG2063) including its own **promoter** and **terminator** was cloned into the shuttle vector pAM401 and used to transform GBS strain **515**

FIG.7B

GBS3 protein is exposed on the **515 (pAM401-SAG2063)** surface at high level as revealed by FACS analysis

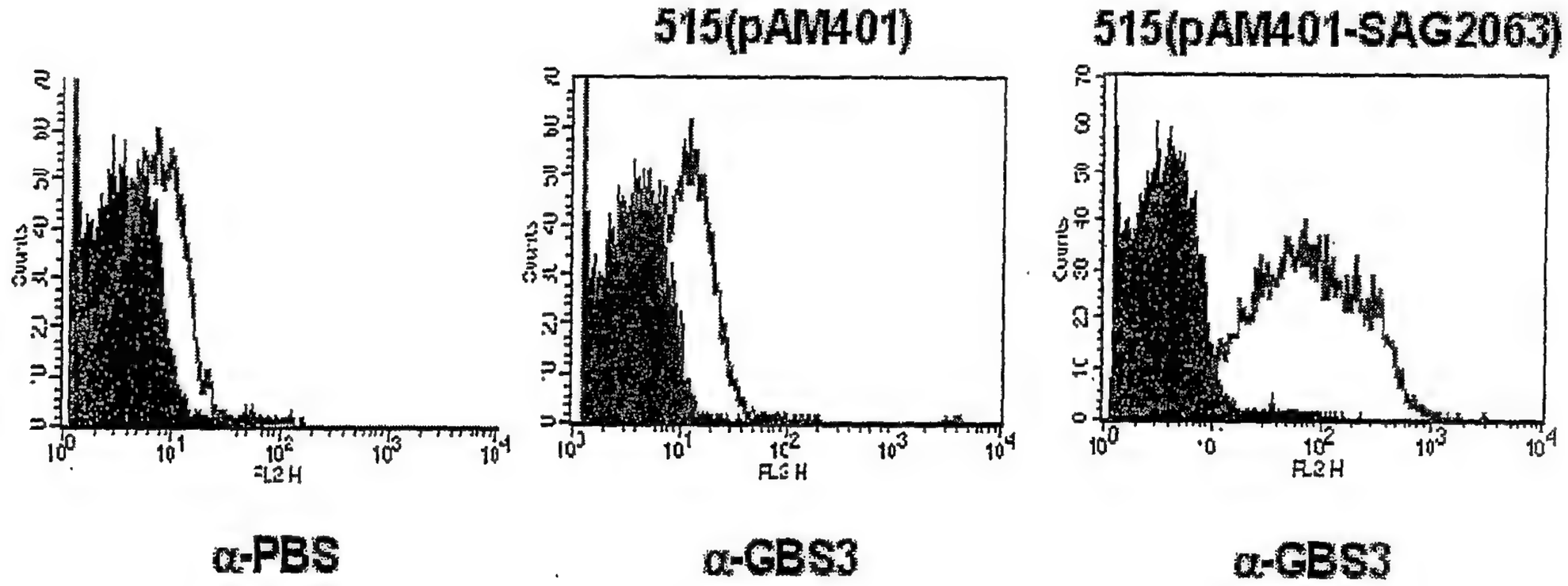
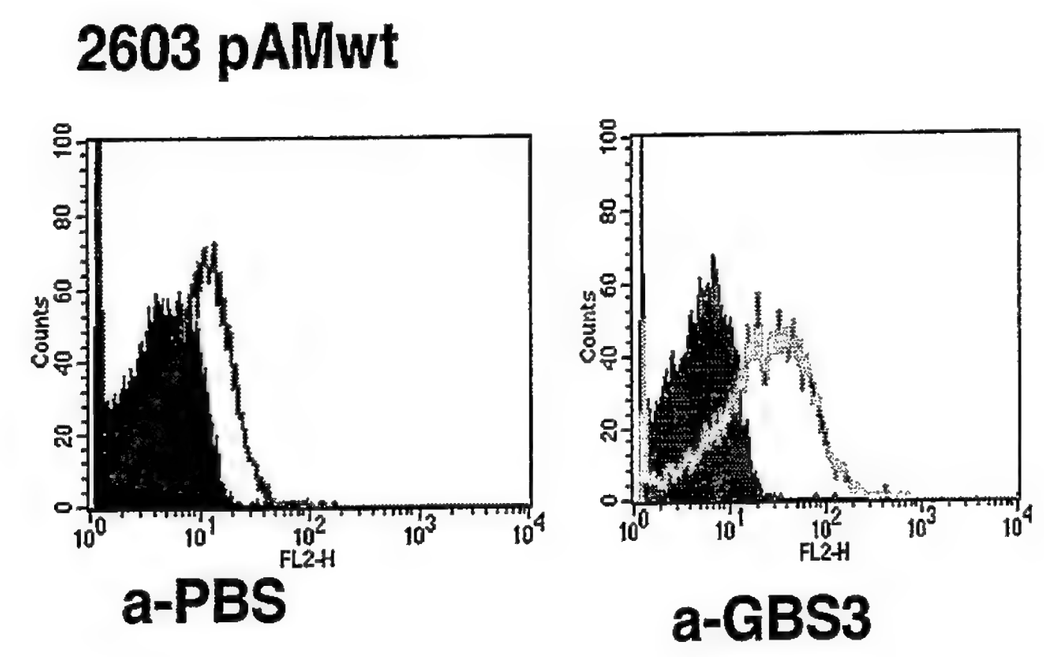
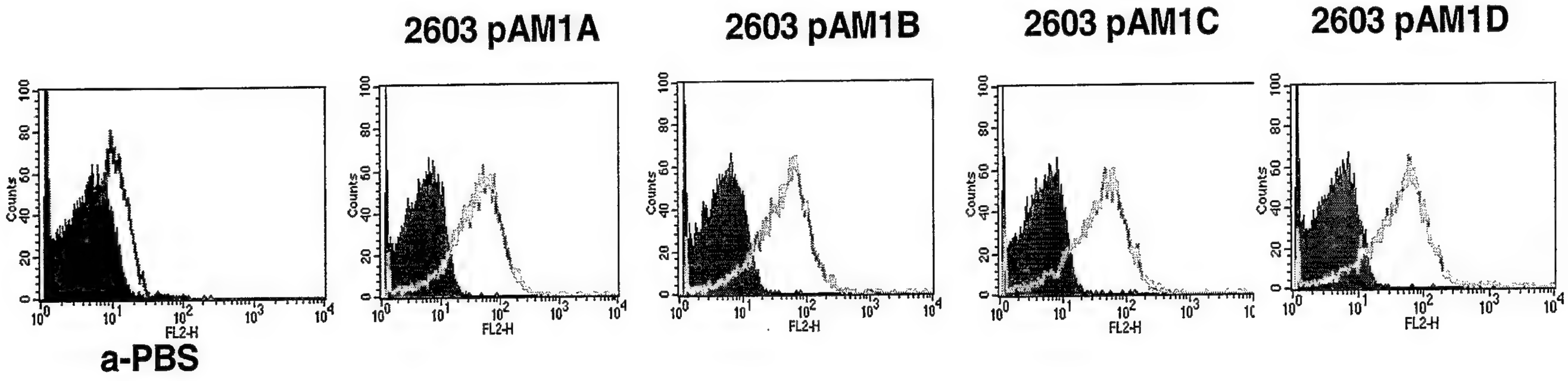


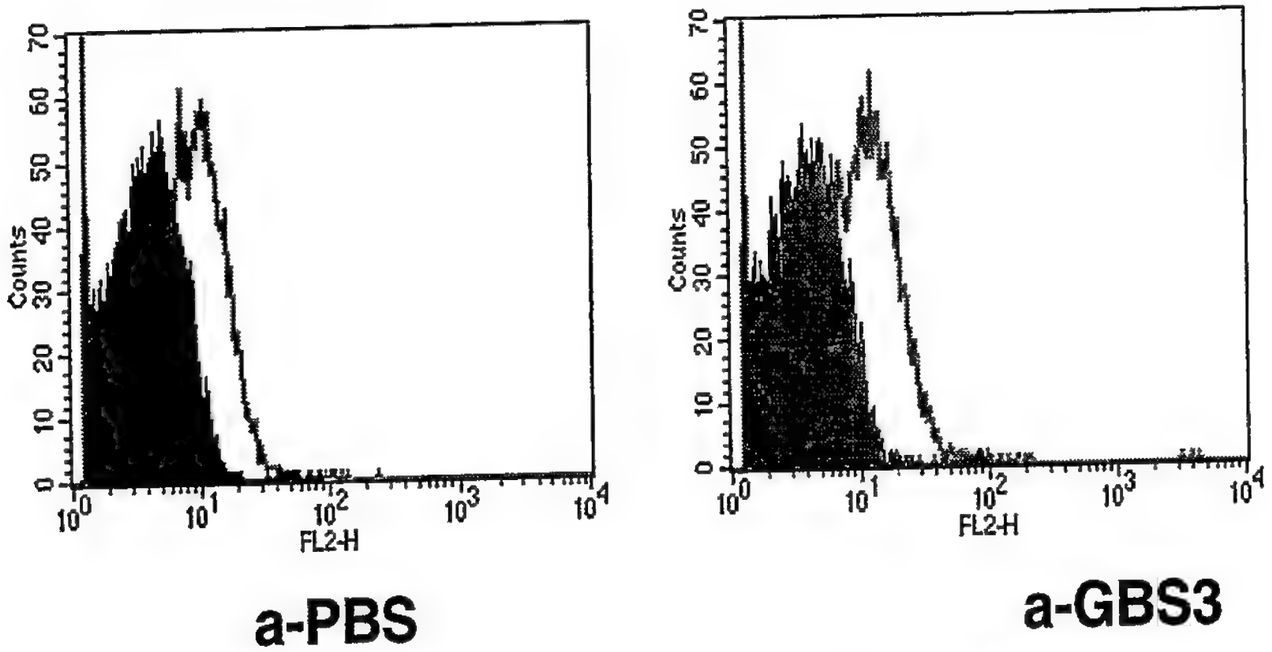
FIG. 8A





GBS Strain	DMean GBS3
2603 pAMwt	184
2603 pAM1A	232
2603 pAM1B	243
2603 pAM1C	239
2603 pAM1D	262

FIG. 8B



GBS Strain	DMean GBS3
515 pAMwt	28
515 pAM1A	276
515 pAM1B	291
515 pAM1C	285

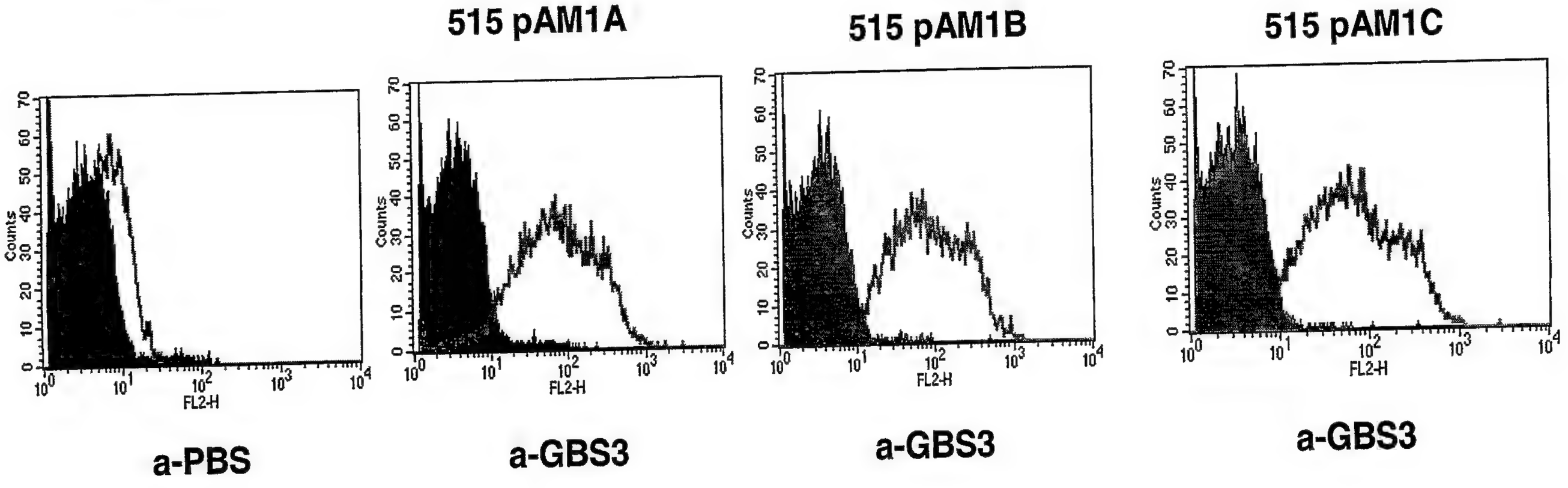
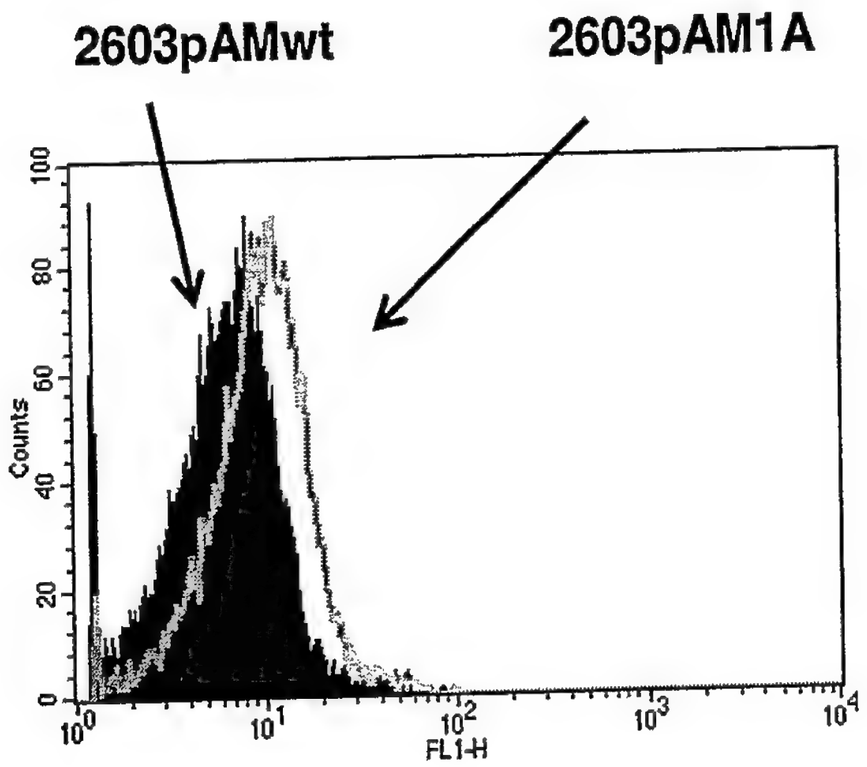
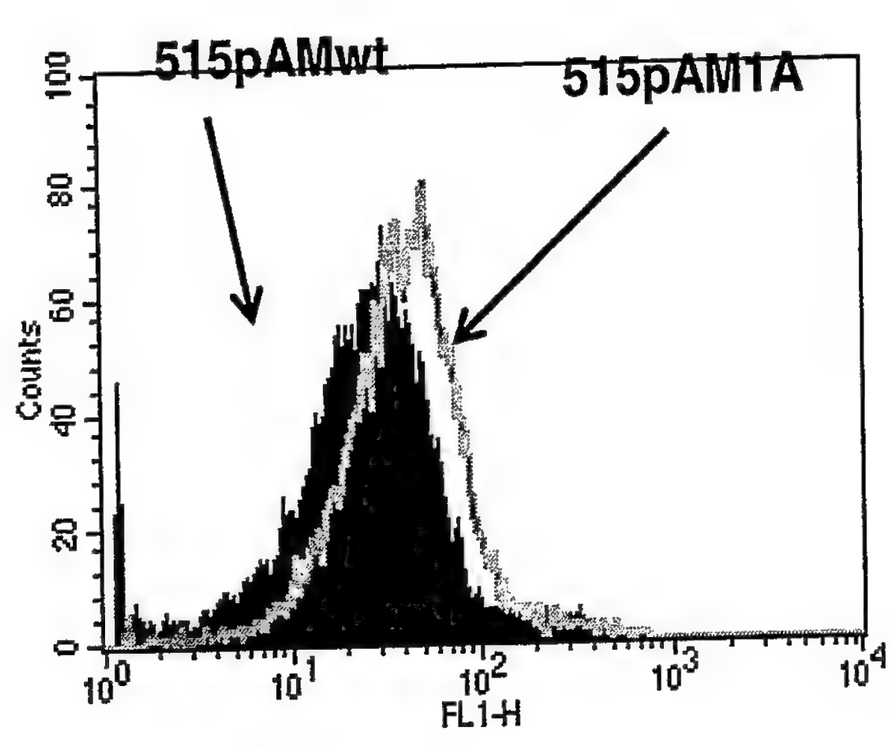
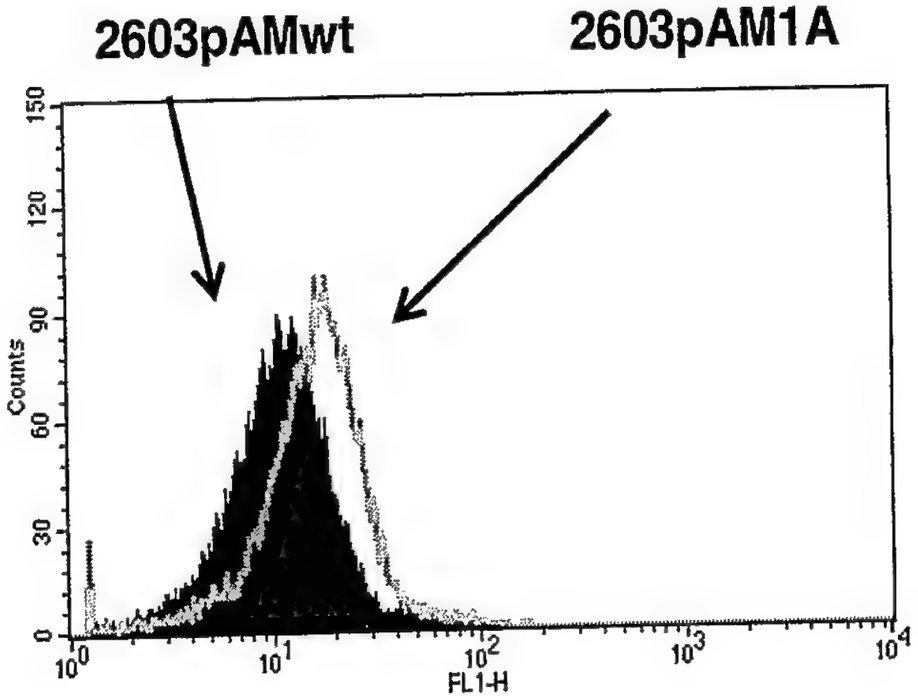


FIG. 9



50 mg/ml





100 mg/ml

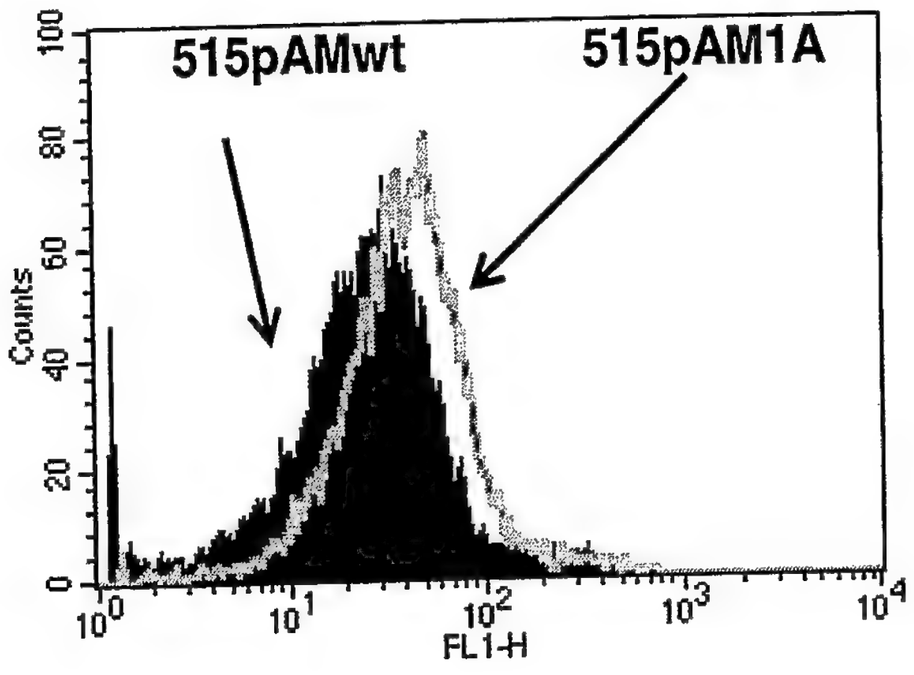
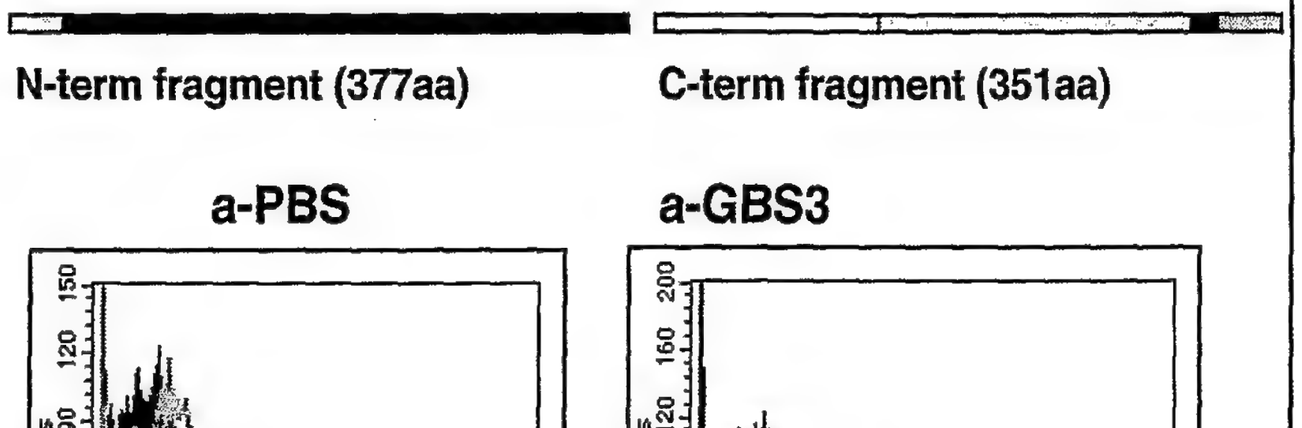


FIG. 10

FIG. 10A

515 type Ia



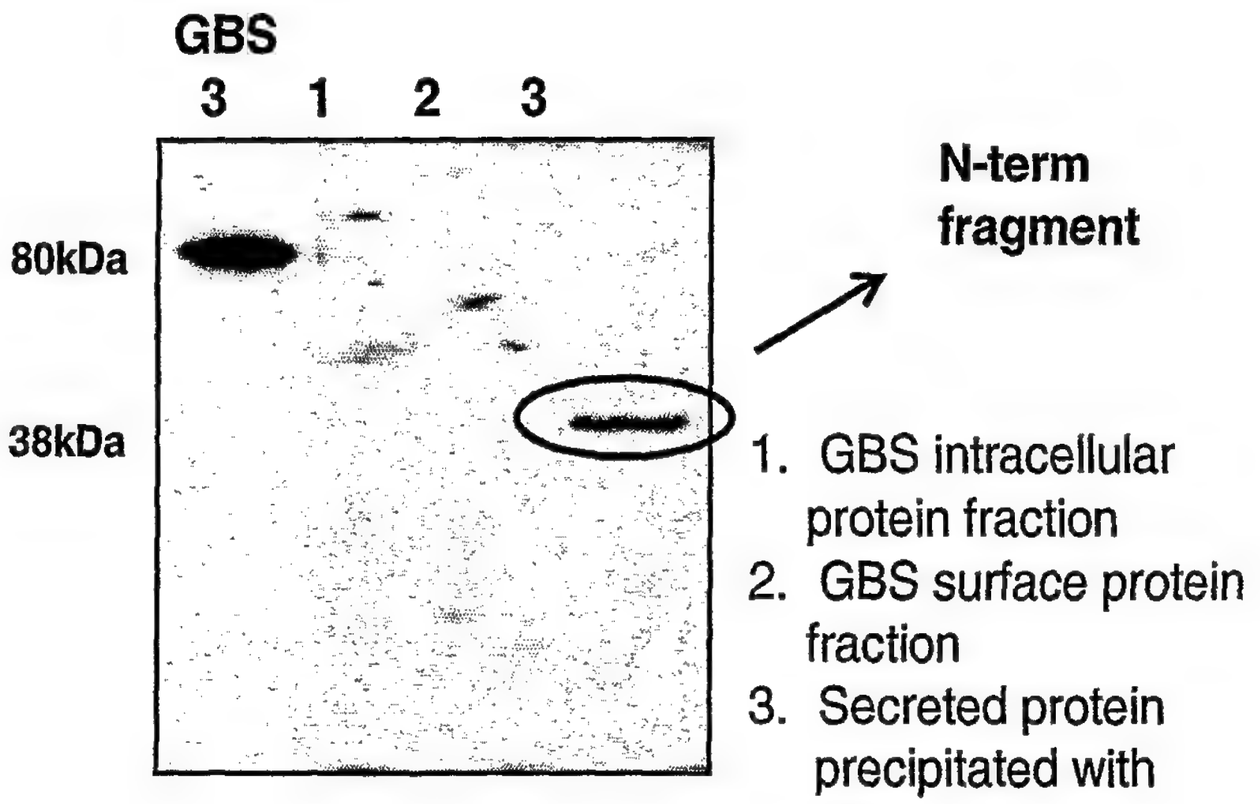
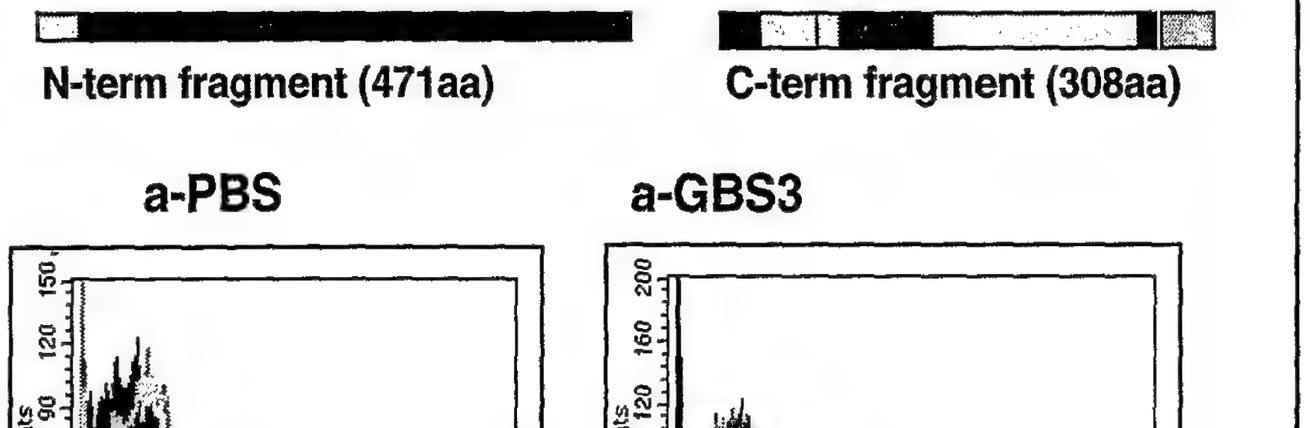


FIG. 10B

CJB111 type V



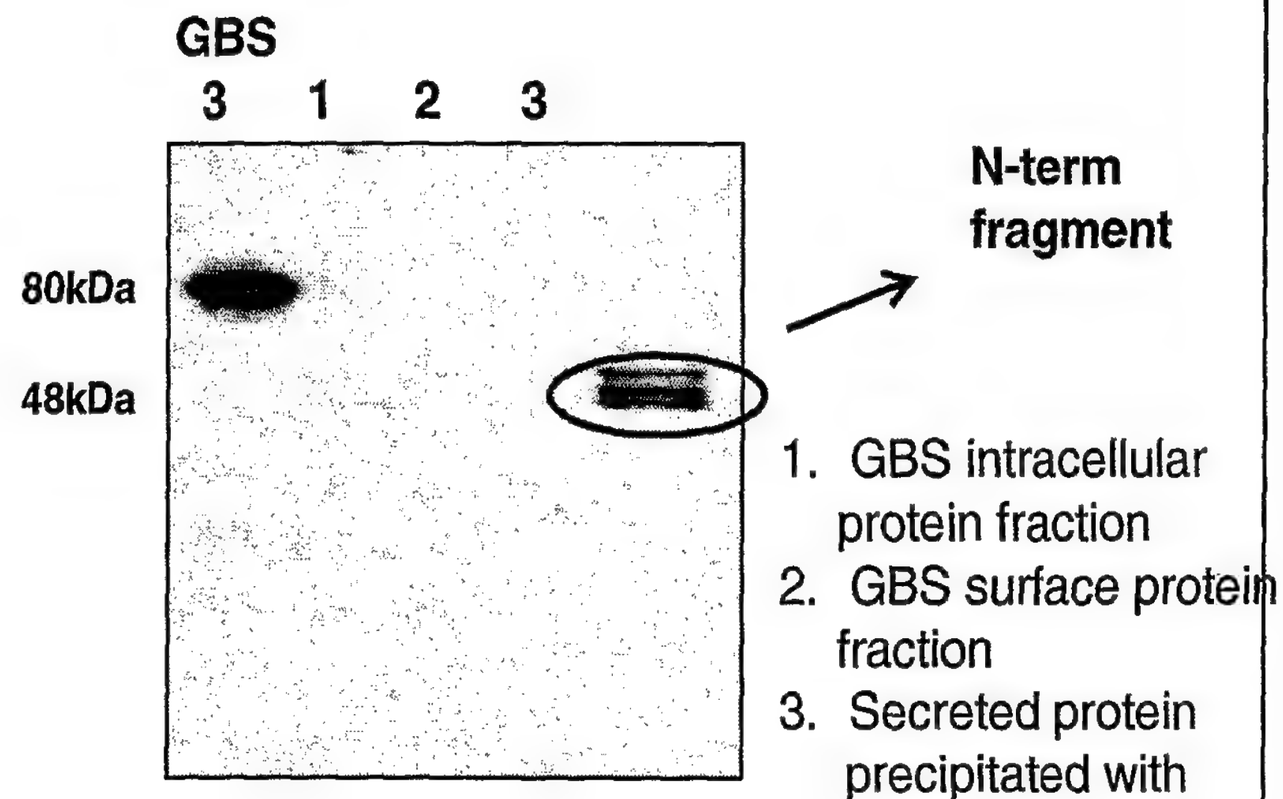
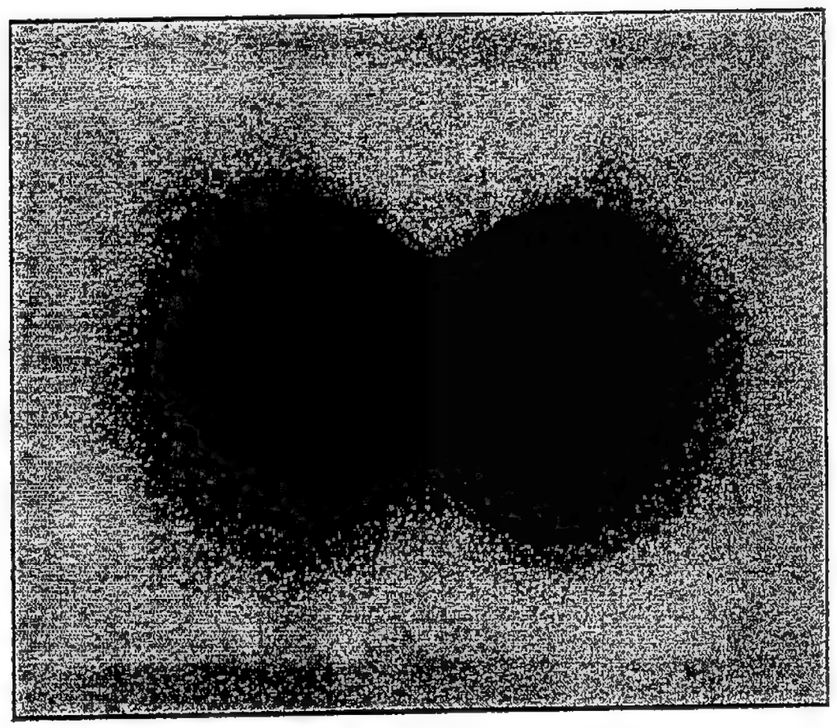
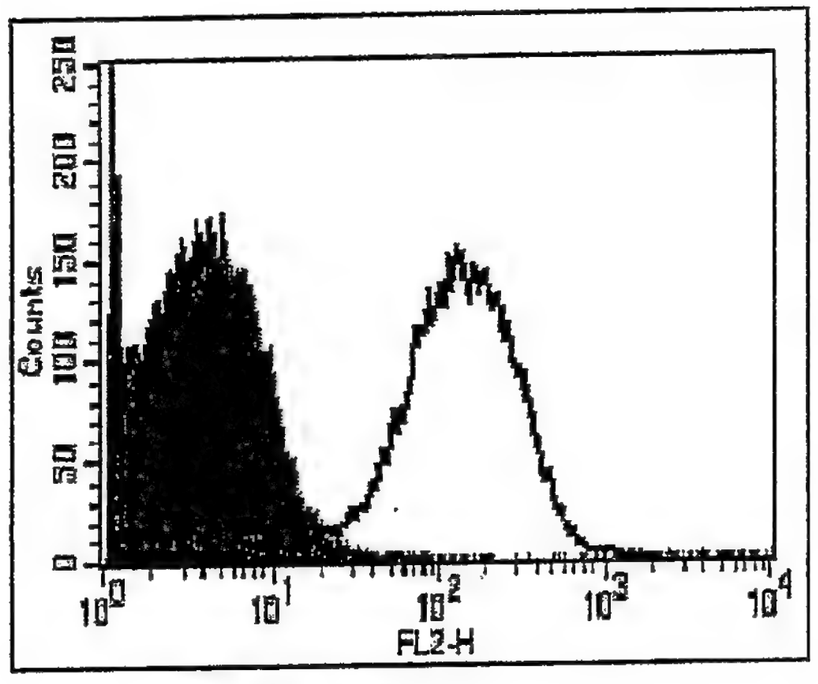


FIG. 10C

Negative control

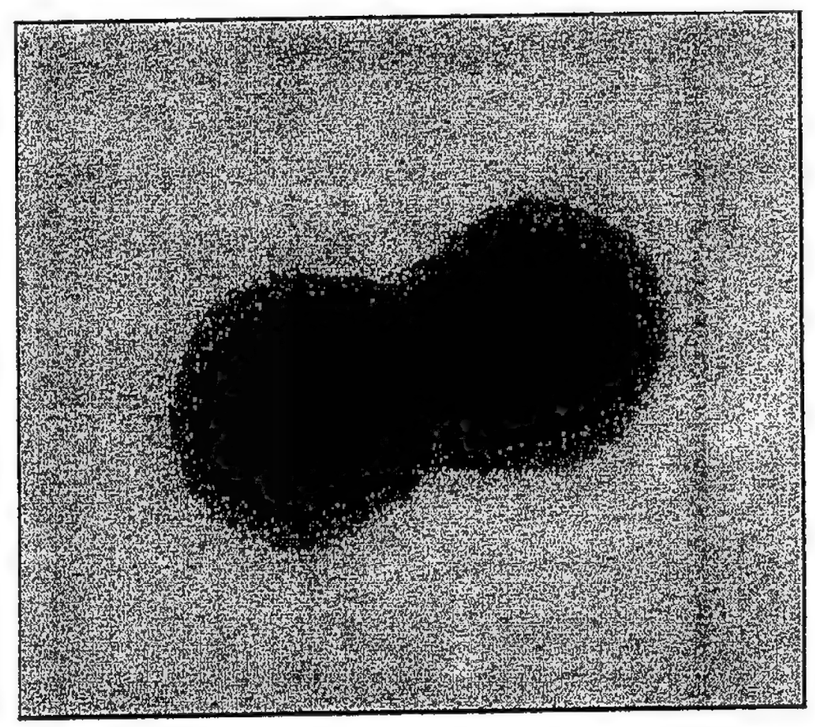


α-GBS3



ΔMean=270

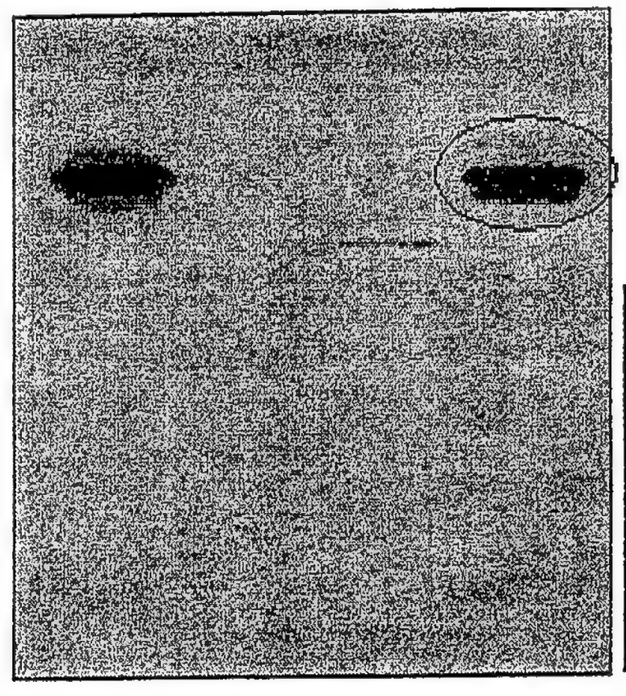
Immuno-gold staining of GBS3 on 2603 V/R strain



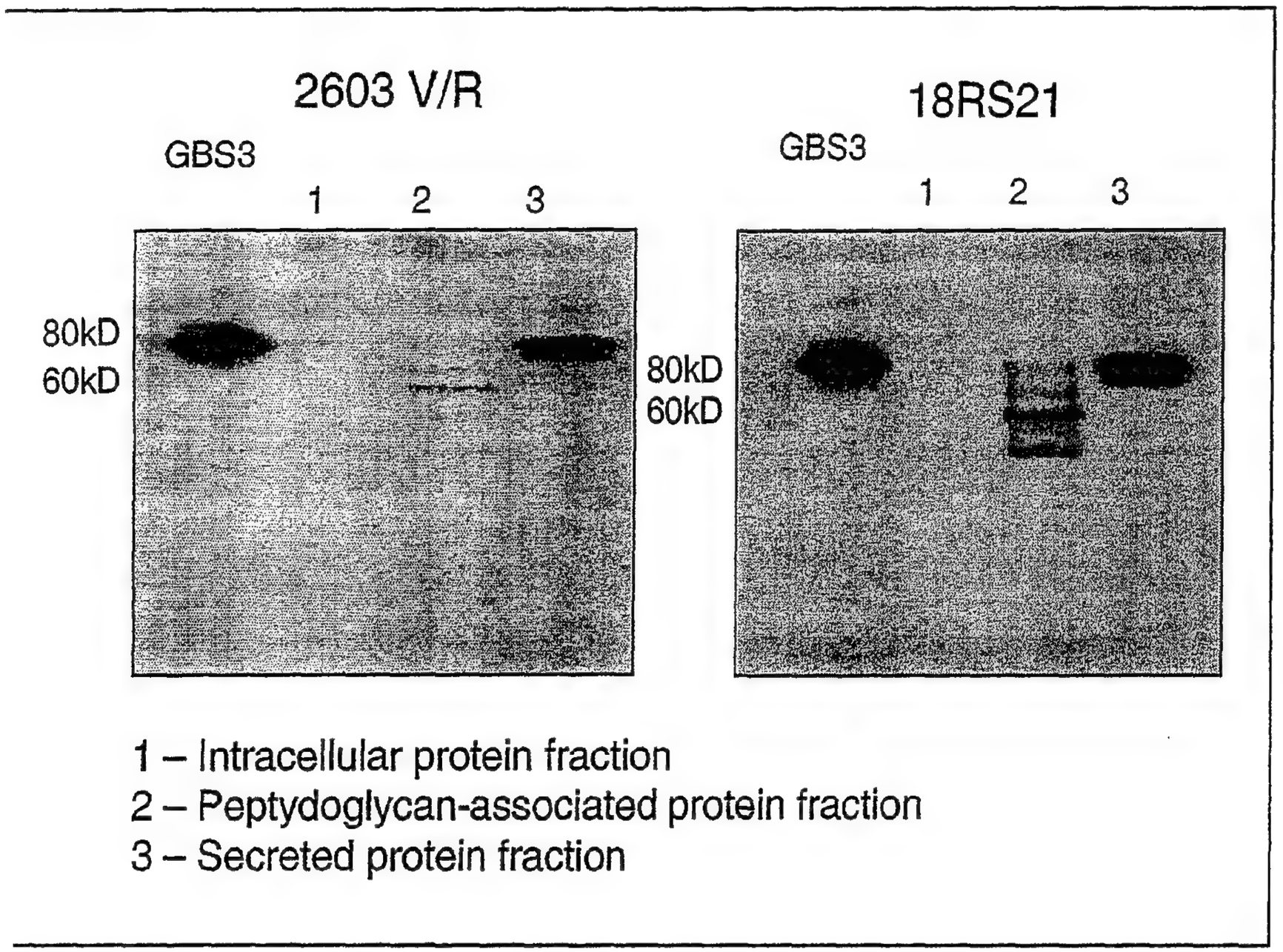
GBS

3 1 2 3

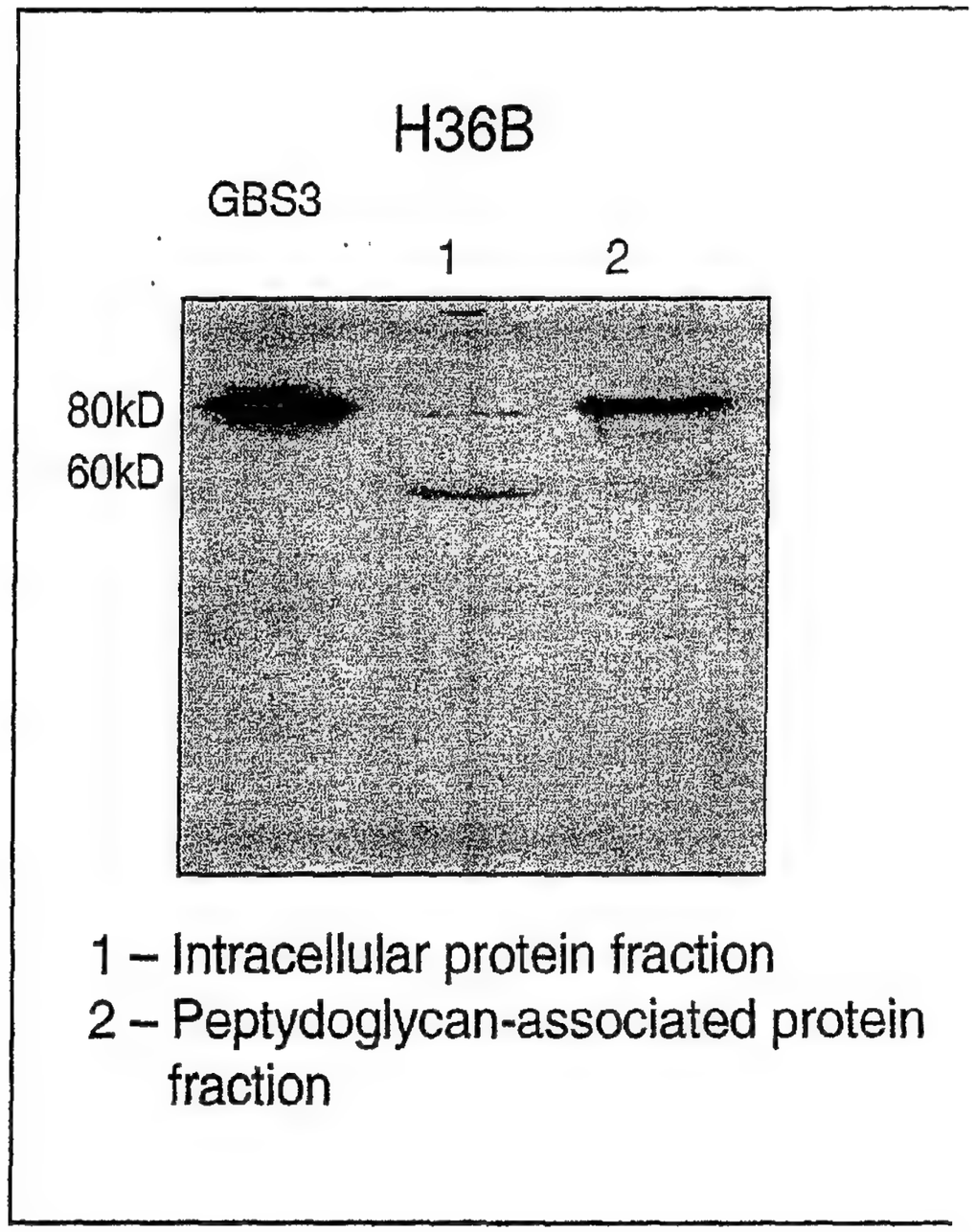
80kDa



1. GBS intracellular protein fraction
2. GBS surface protein fraction
3. Secreted protein precipitated with TCA


2603 V/R
GBS3
1
2
3
80kD
60kD
18RS21
GBS3
1
2
3
80kD
60kD
1 – Intracellular protein fraction
2 – Peptydoglycan-associated protein fraction
3 – Secreted protein fraction

10D


H36B
GBS3
1
2
80kD
60kD
1 – Intracellular protein fraction
2 – Peptydoglycan-associated protein fraction

10E

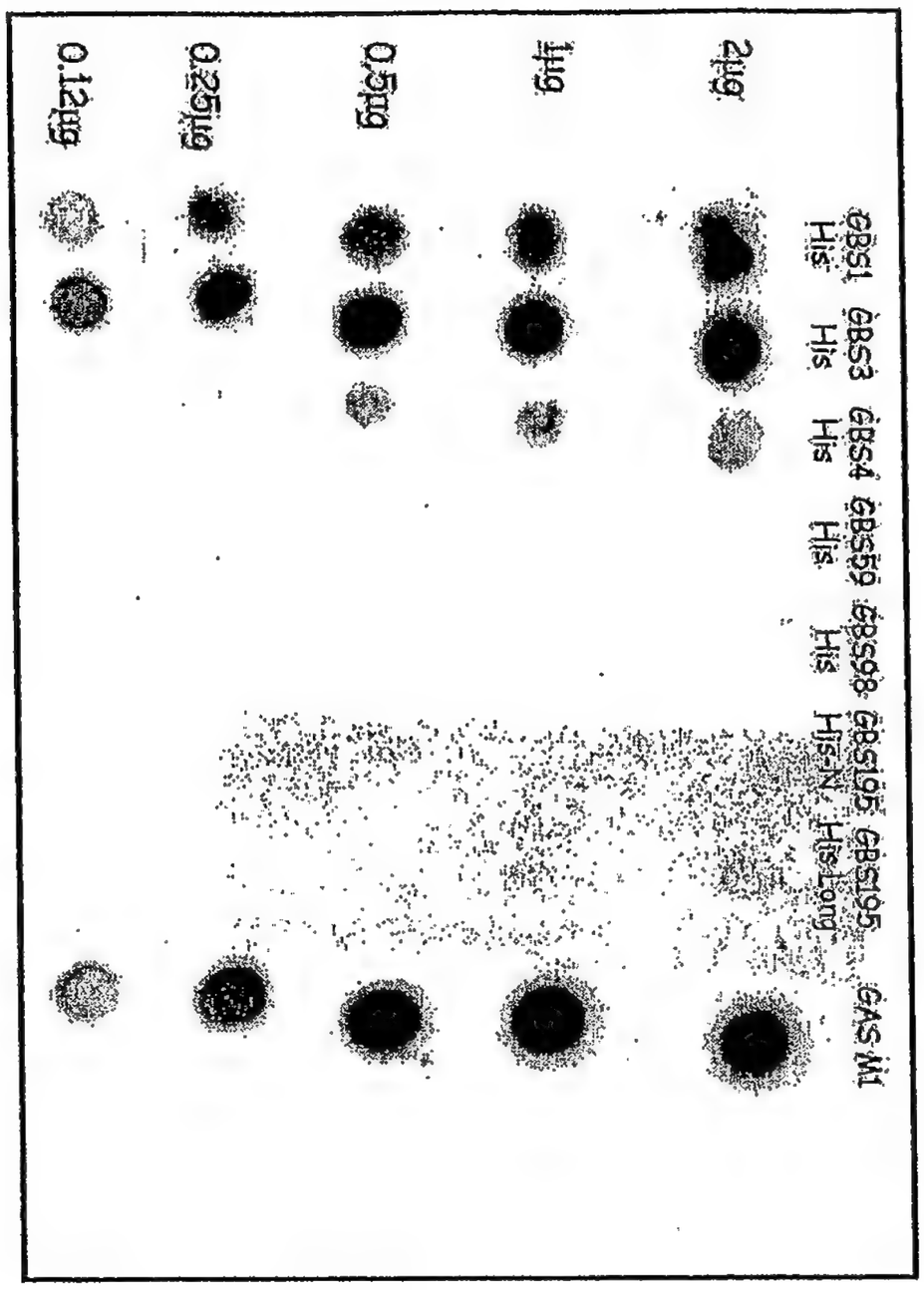

GBS1 His
GBS3 His
GBS4 His
GBS59 His
GBS98 His
GBS195 His-N
GBS195 His-Long
GAS M1
2µg
1µg
0.5µg
0.25µg
0.12µg

FIG. 11A

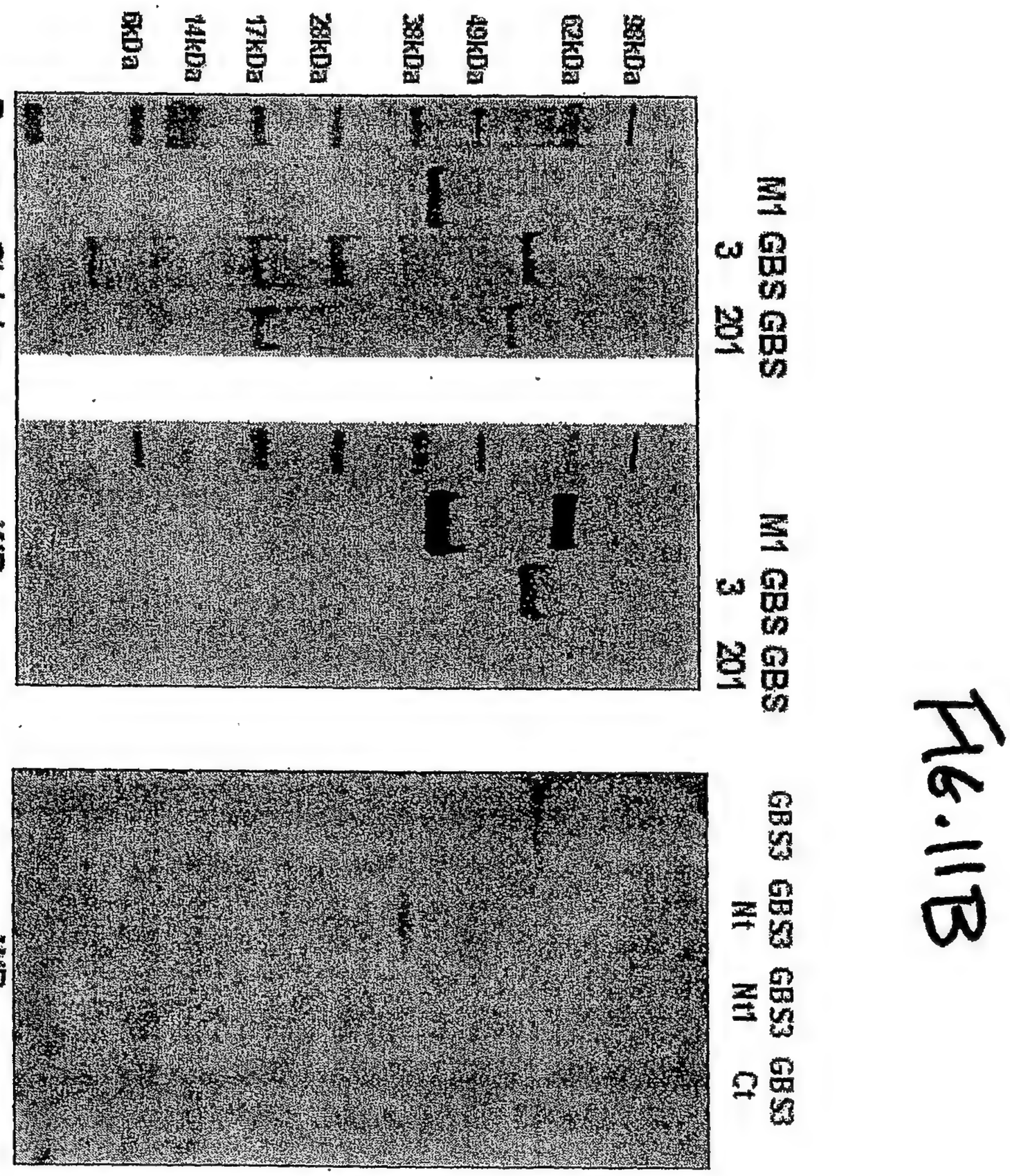

M1 GBS GBS
3 201
M1 GBS GBS
3 201
98kDa
62kDa
49kDa
38kDa
28kDa
17kDa
14kDa
6kDa
Ponceau Staining
WB
WB
GBS3 GBS3 GBS3 GBS3 GBS3
M1 M1 Ct

FIG. 11B

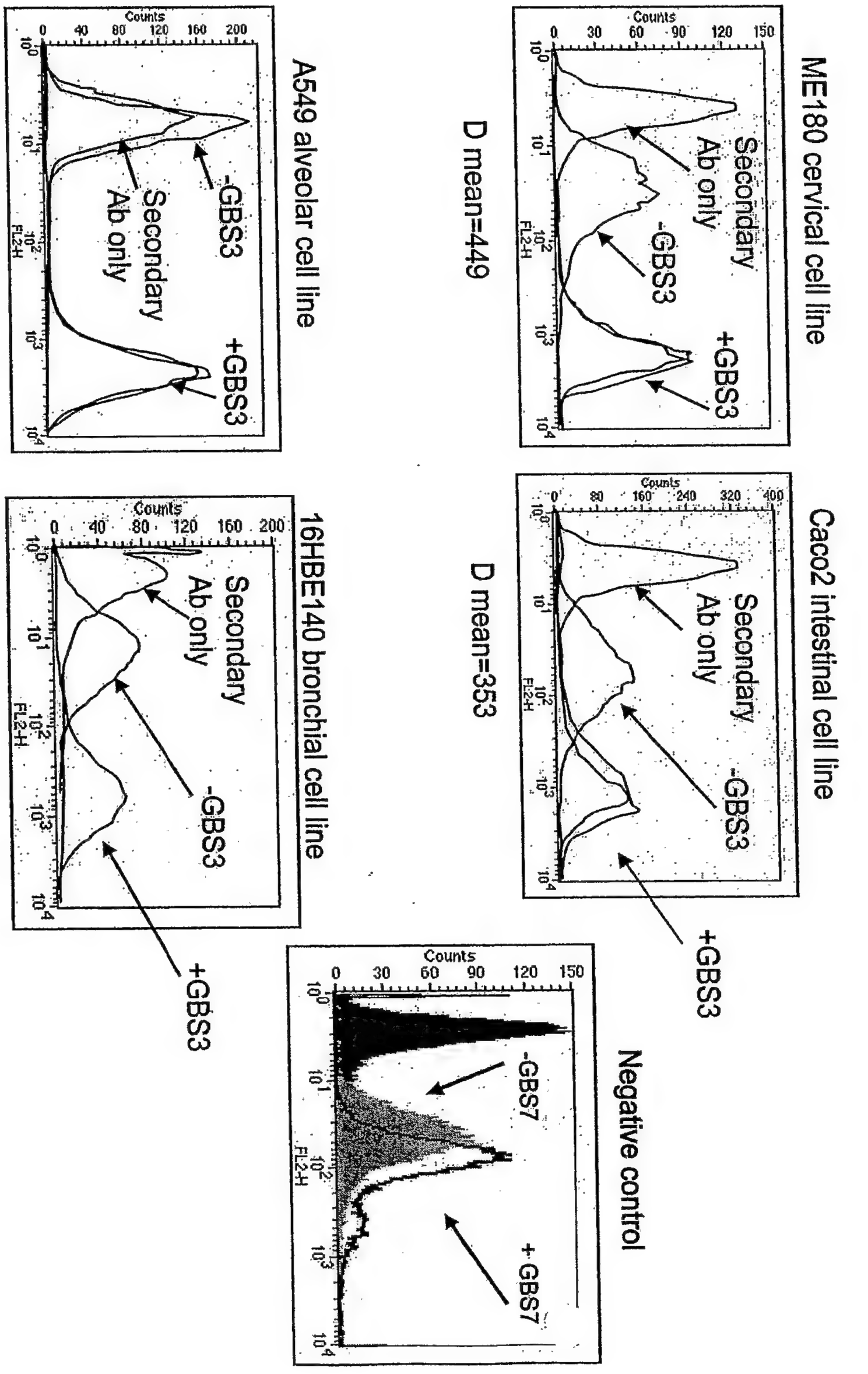

ME180 cervical cell line
Counts
Secondary Ab only
+GBS3
-GBS3
D mean=449
Caco2 intestinal cell line
D mean=353
A549 alveolar cell line
-GBS3
+GBS3
Secondary Ab only
D mean=645
16HBE140 bronchial cell line
D mean=409
Negative control
-GBS7
+GBS7
FL2-H

FIG. 12

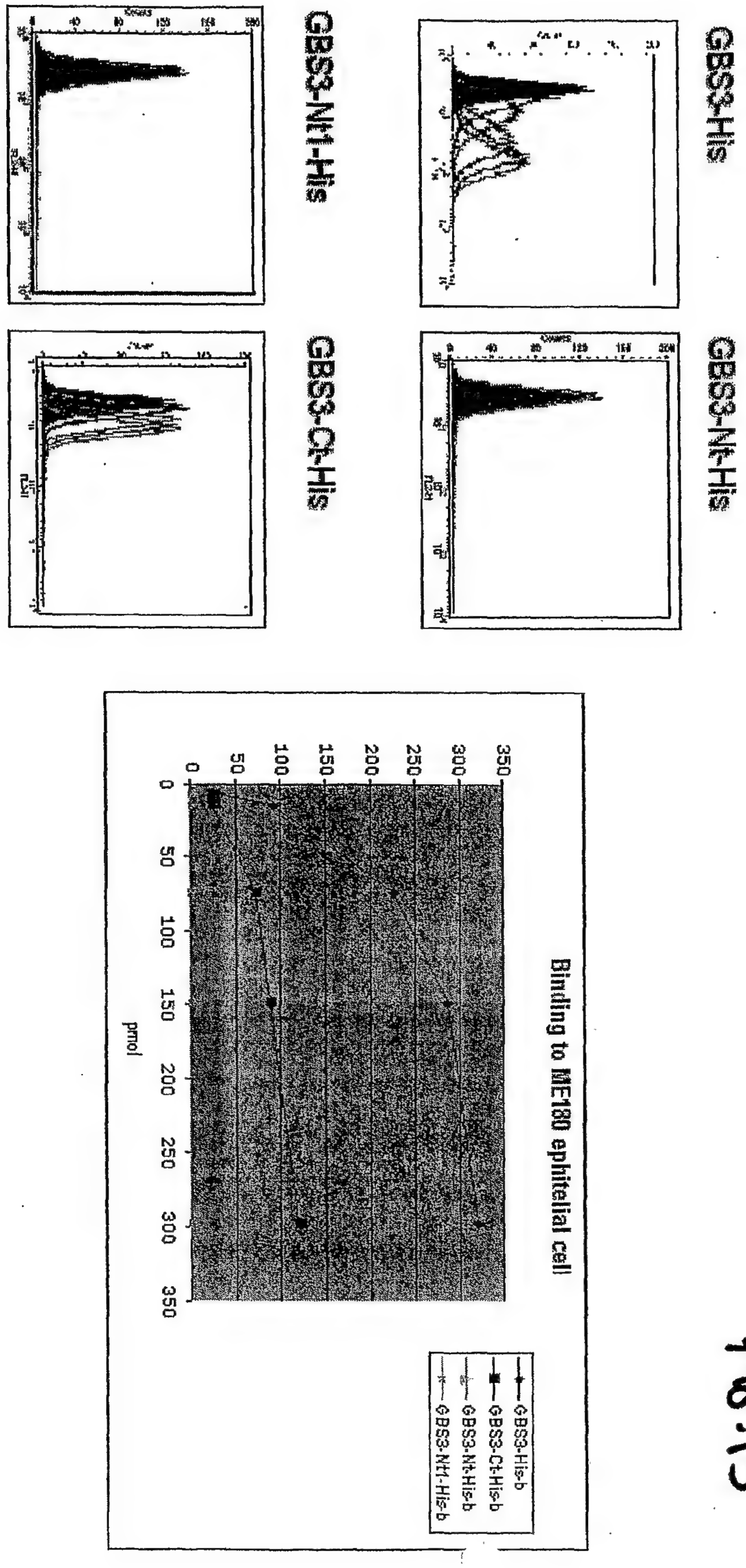

GBS3-Nt1-His
GBS3-His
GBS3-Nt-His
GBS3-Ct-His
Binding to ME180 ephitelial cell
GBS3-His-b
GBS3-Ct-His-b
GBS3-Nt-His-b
GBS3-Nt1-His-b
0
50
100
150
200
250
300
350
pmol

FIG. 13

FIG. 14

FIG. 14A

FIG. 14B

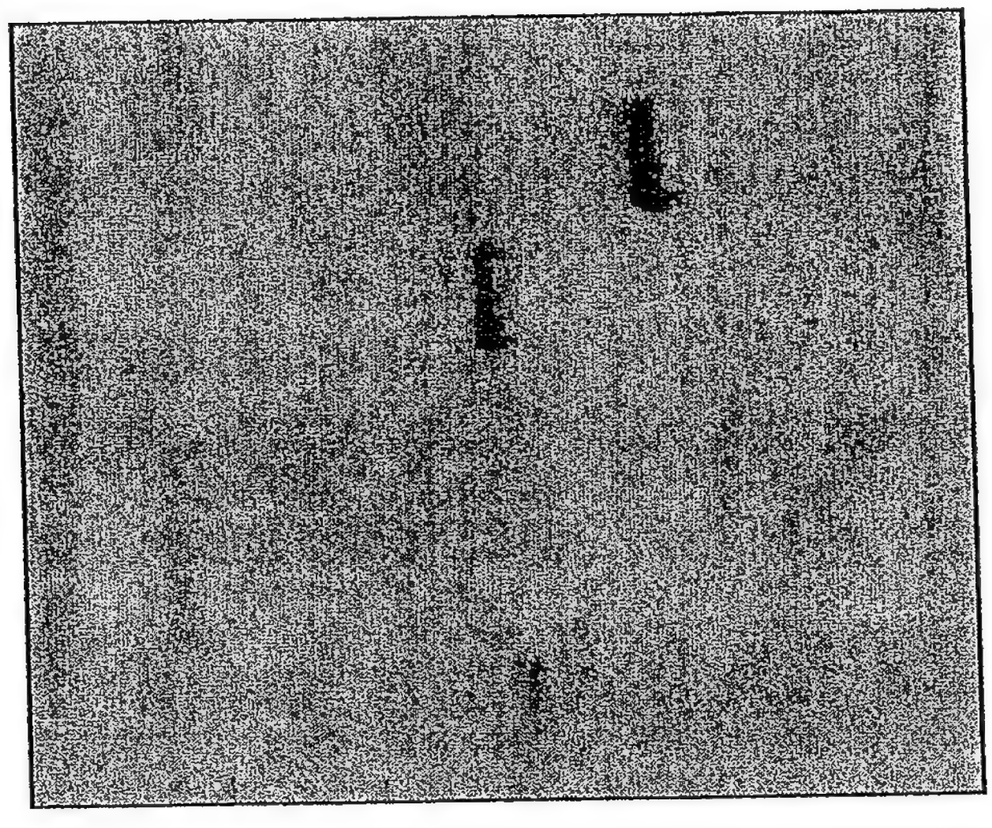
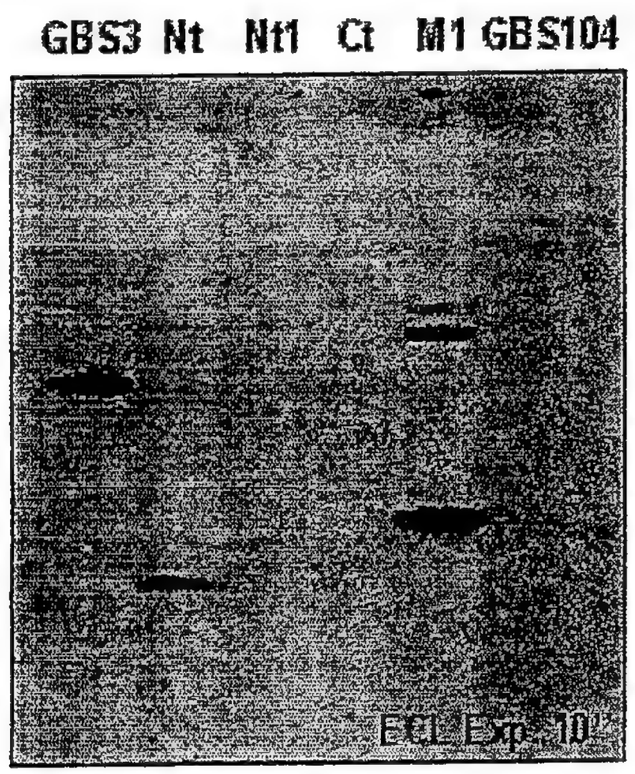
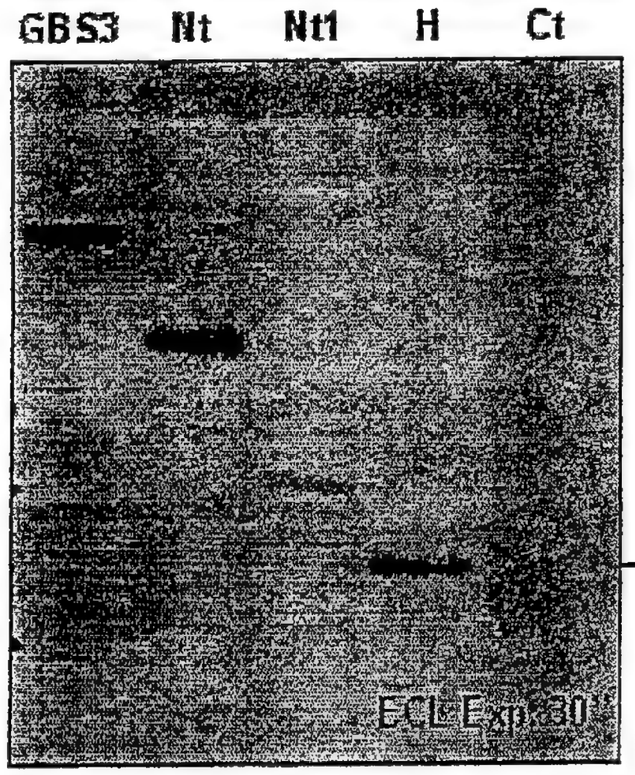


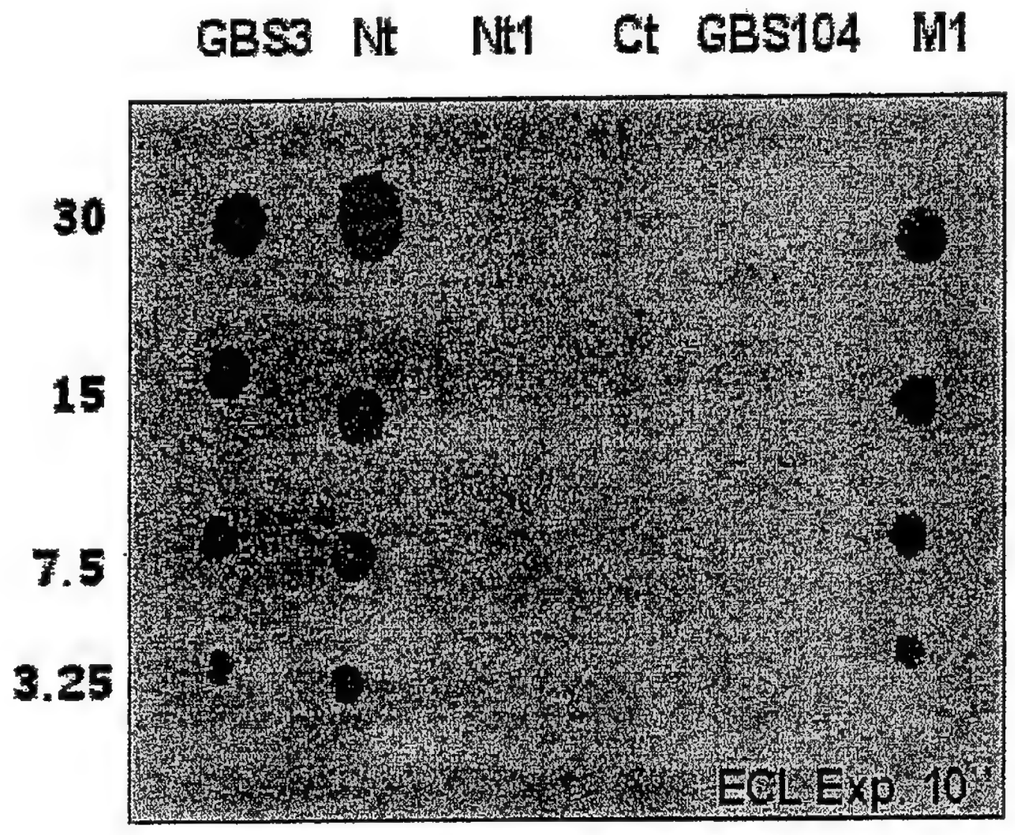
FIG. 14C

FIG. 15





Western blot analysis of denatured GBS3 protein (15pMol) overlaid with 5 µg/ml of purified human-IgA-HRP



Dot Blot analysis of native GBS3 protein (pMol) overlaid with 5 µg/ml of purified human-IgA-HRP.

The binding region appears to be contained within the first 200 aminoacids.

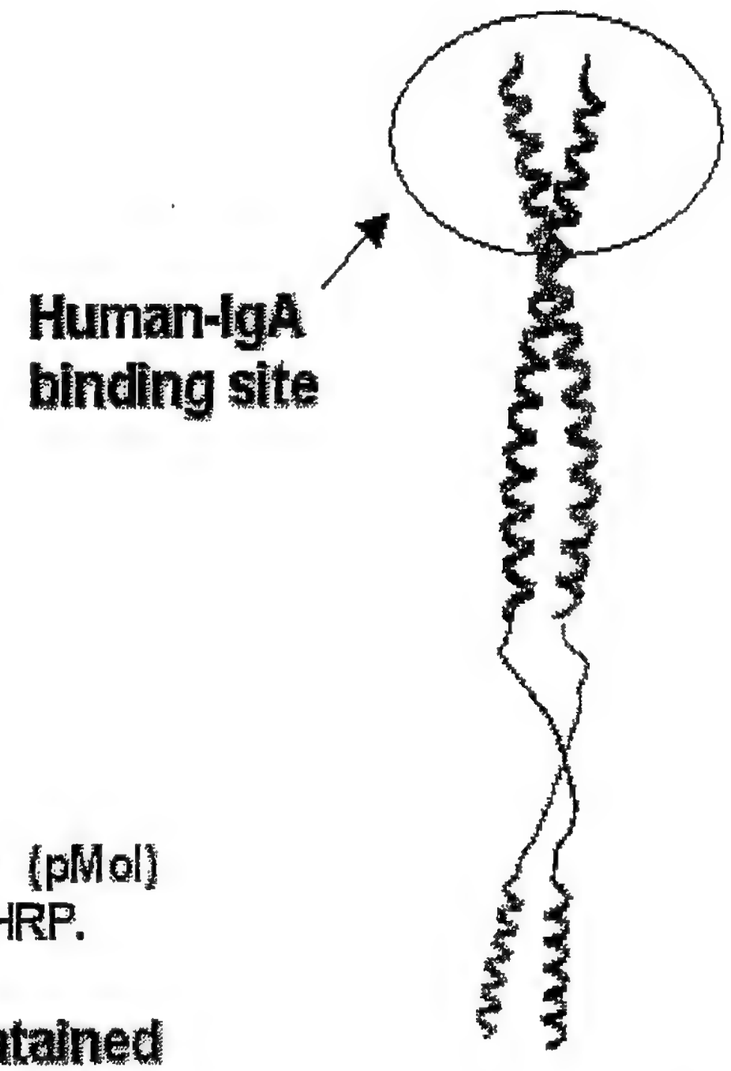
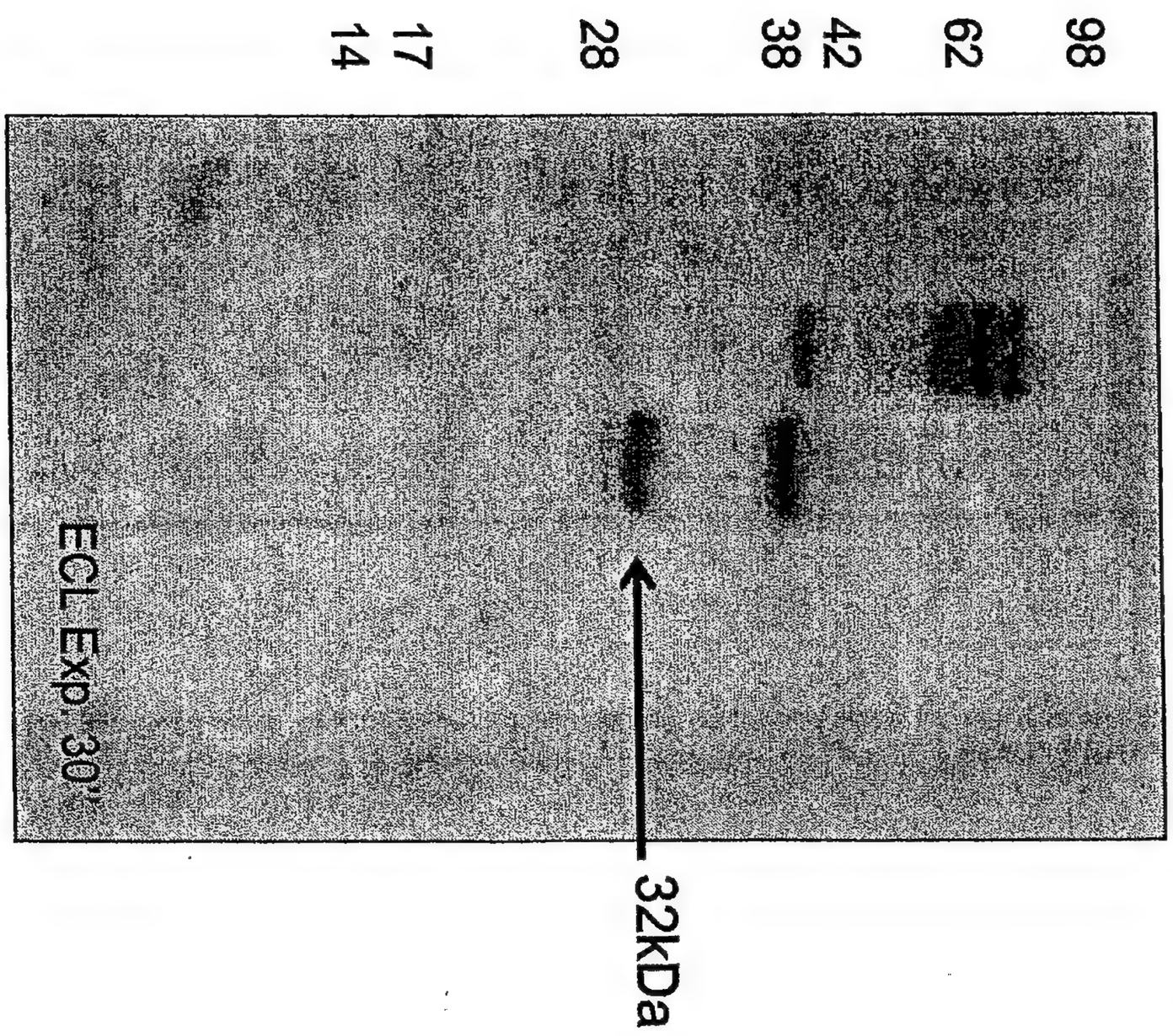


FIG. 16



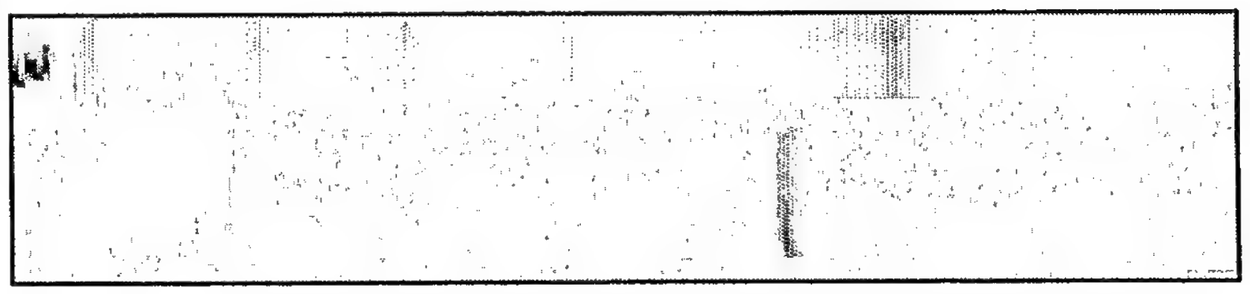


FIG. 17A

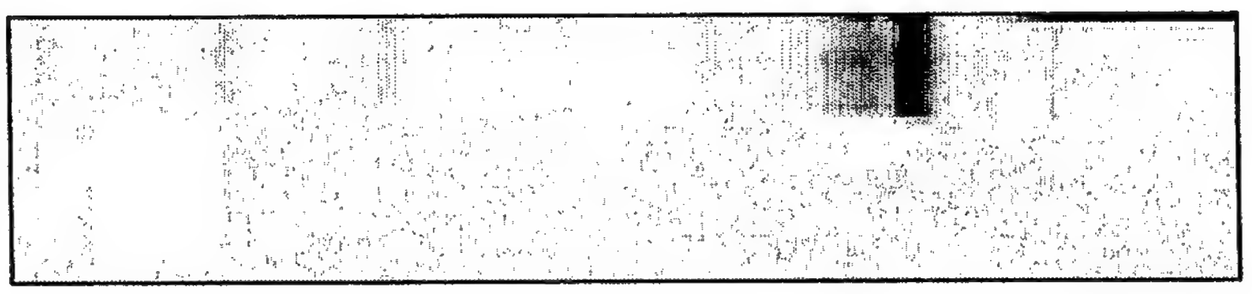


FIG. 17B

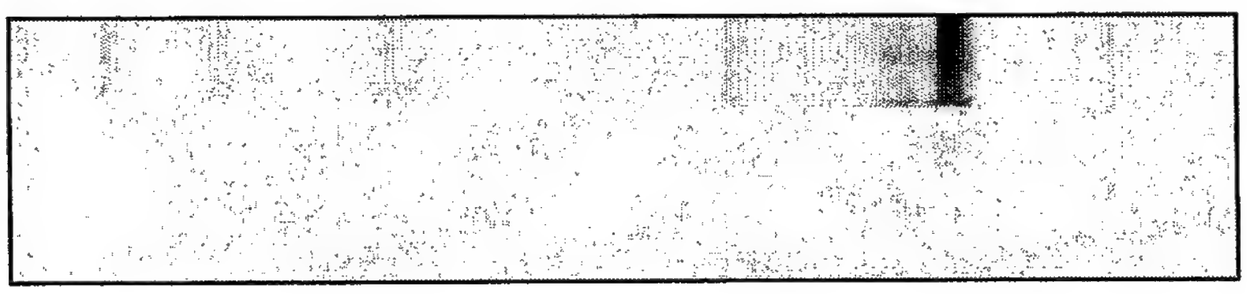


FIG. 17C

FIG. 17

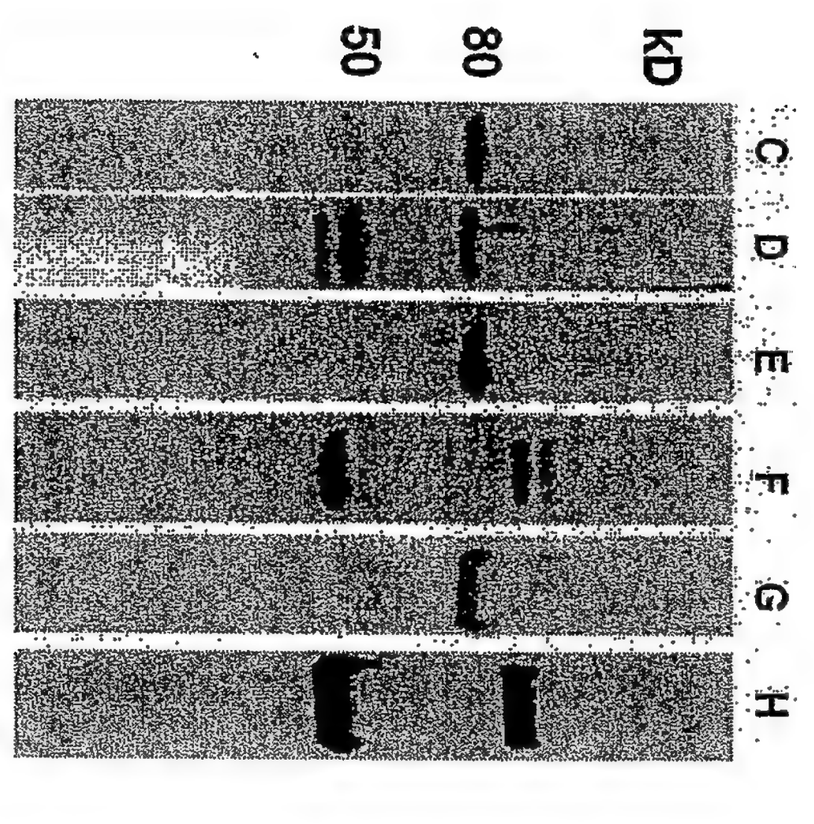


FIG. 18

Fig. 19

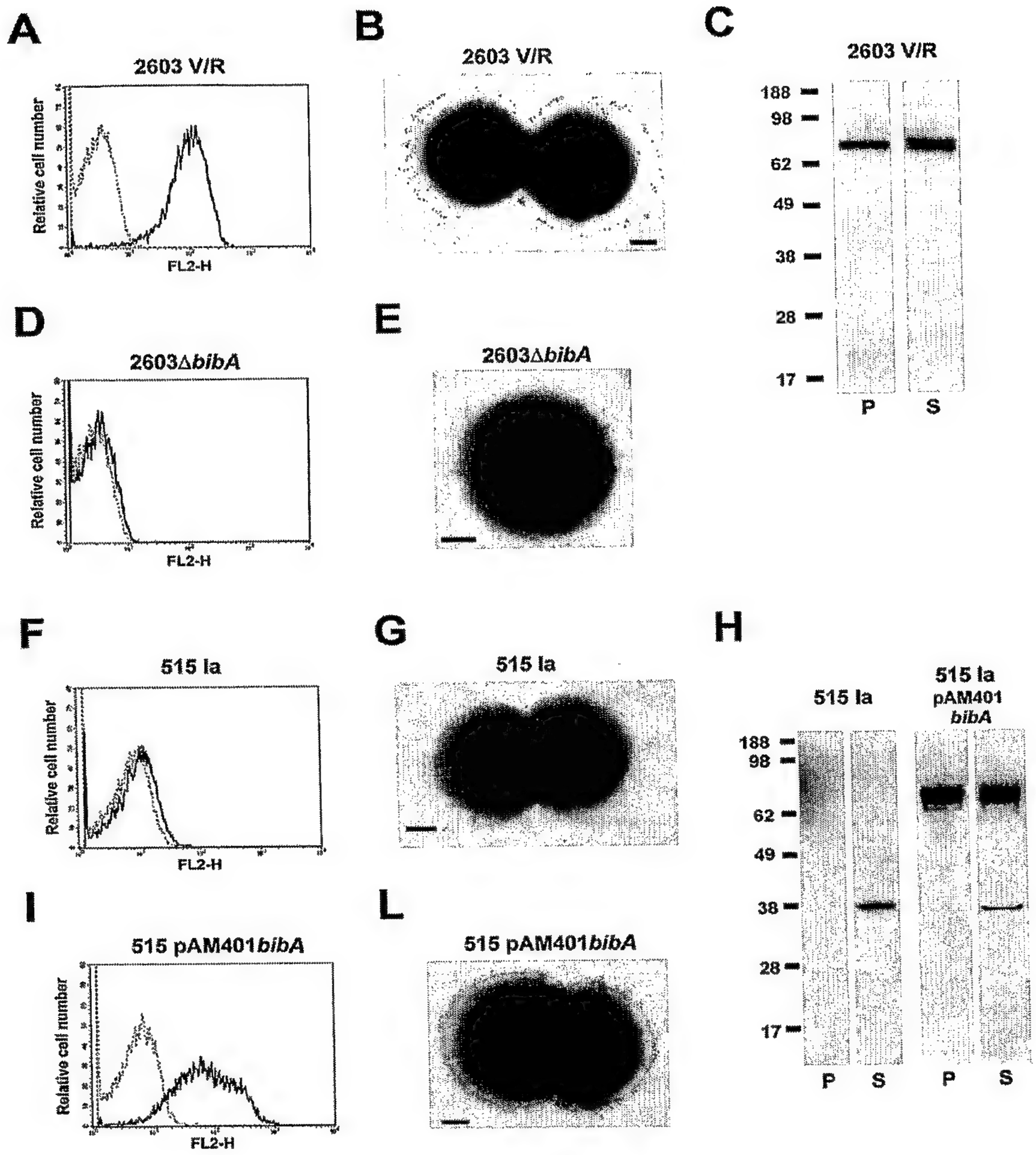

A
2603 V/R
Relative cell number
FL2-H
B
2603 V/R
C
2603 V/R
188
98
62
49
38
28
17
P
S
D
2603Δ*bibA*
Relative cell number
FL2-H
E
2603Δ*bibA*
F
515 Ia
Relative cell number
FL2-H
G
515 Ia
H
515 Ia
515 Ia pAM401 *bibA*
188
98
62
49
38
28
17
P
S
P
S
I
515 pAM401*bibA*
Relative cell number
FL2-H
L
515 pAM401*bibA*

Fig. 20

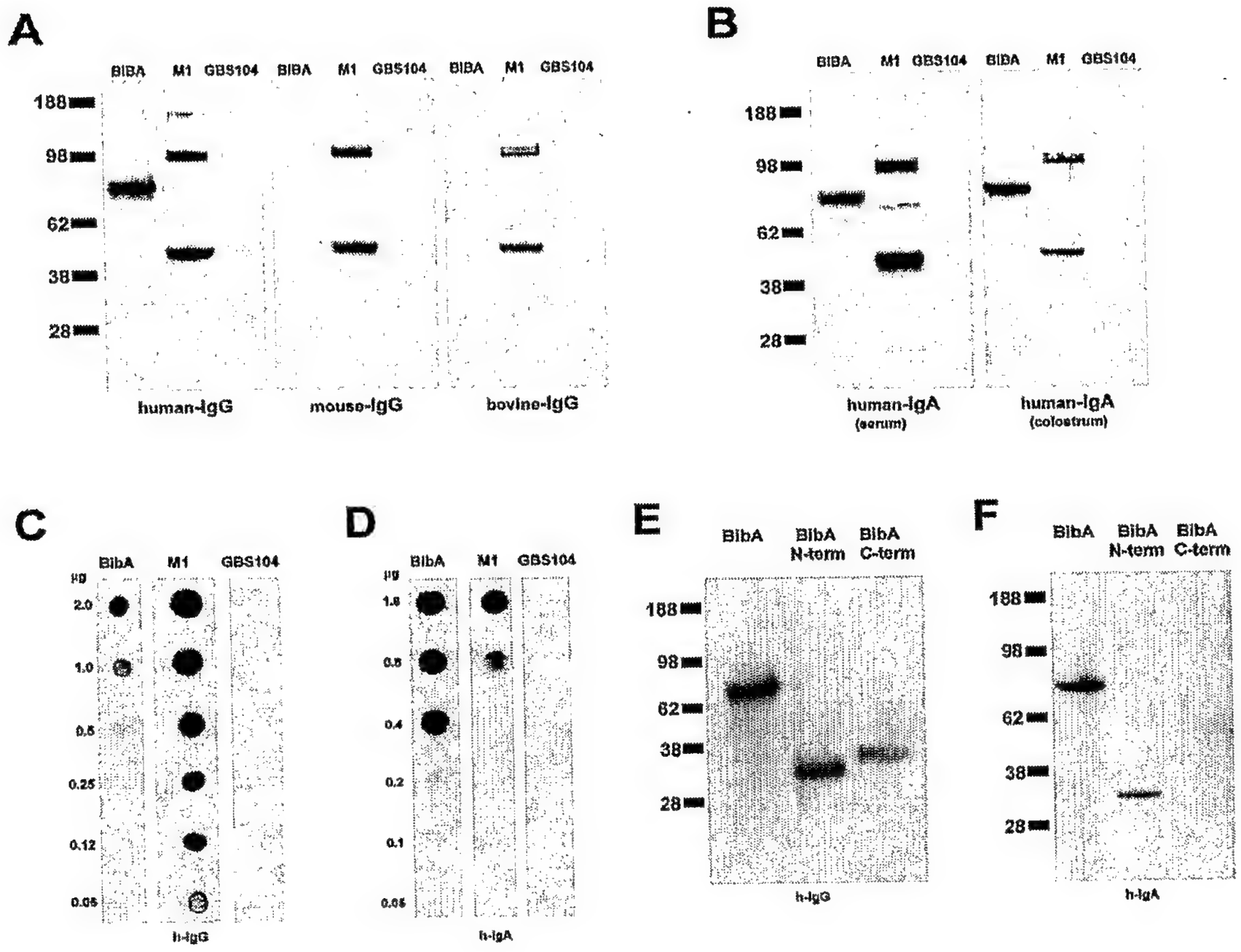

A
BIBA M1 GBS104 BIBA M1 GBS104 BIBA M1 GBS104
188
98
62
38
28
human-IgG
mouse-IgG
bovine-IgG
B
BIBA M1 GBS104 BIBA M1 GBS104
188
98
62
38
28
human-IgA (serum)
human-IgA (colostrum)
C
BibA M1 GBS104
µg
2.0
1.0
0.5
0.25
0.12
0.05
h-IgG
D
BibA M1 GBS104
µg
1.6
0.8
0.4
0.2
0.1
0.05
h-IgA
E
BibA BibA N-term BibA C-term
188
98
62
38
28
h-IgG
F
BibA BibA N-term BibA C-term
188
98
62
38
28
h-IgA

Fig. 21

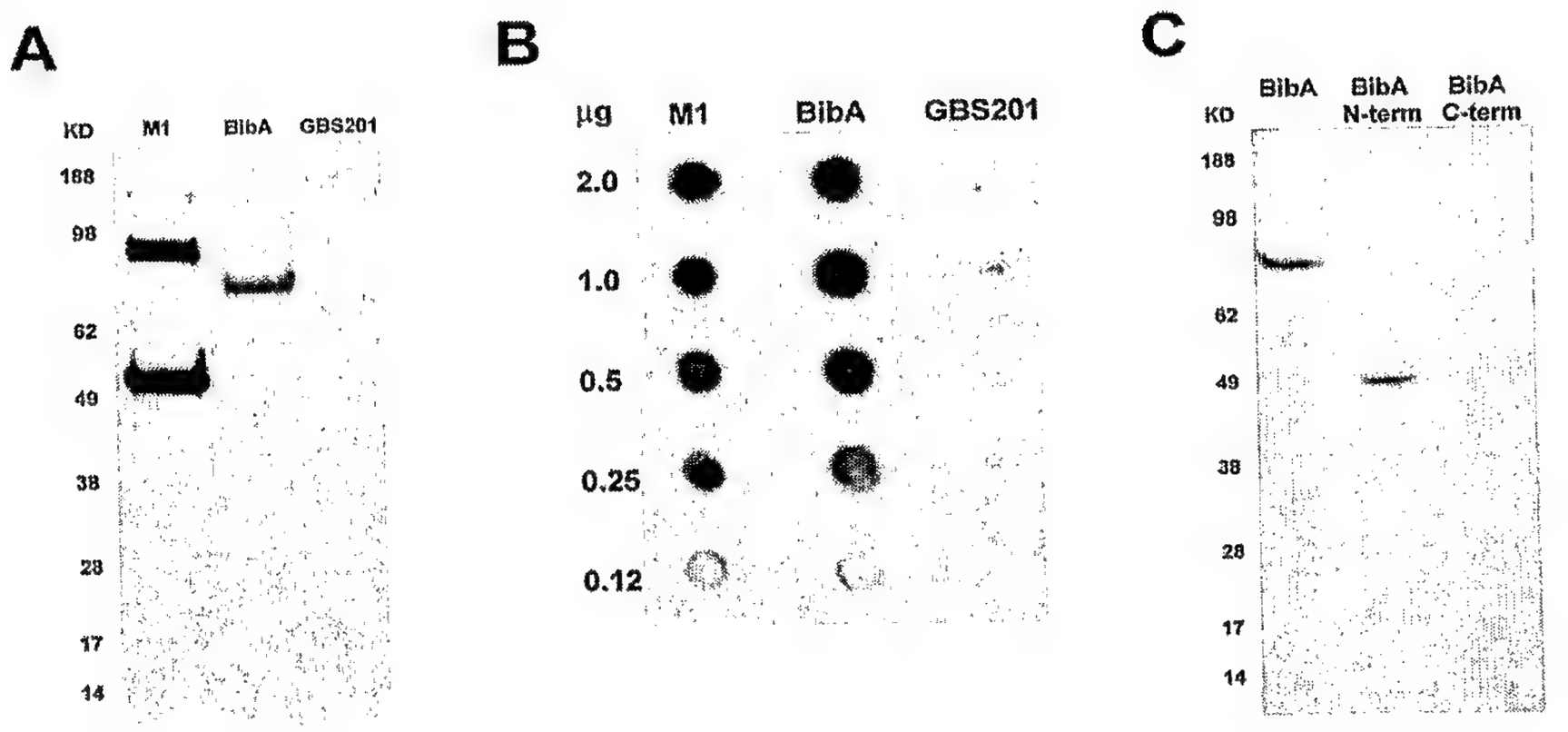

A
KD
M1
BibA
GBS201
188
98
62
49
38
28
17
14
B
µg
M1
BibA
GBS201
2.0
1.0
0.5
0.25
0.12
C
BibA
BibA N-term
BibA C-term
KD
188
98
62
49
38
28
17
14

Fig. 22

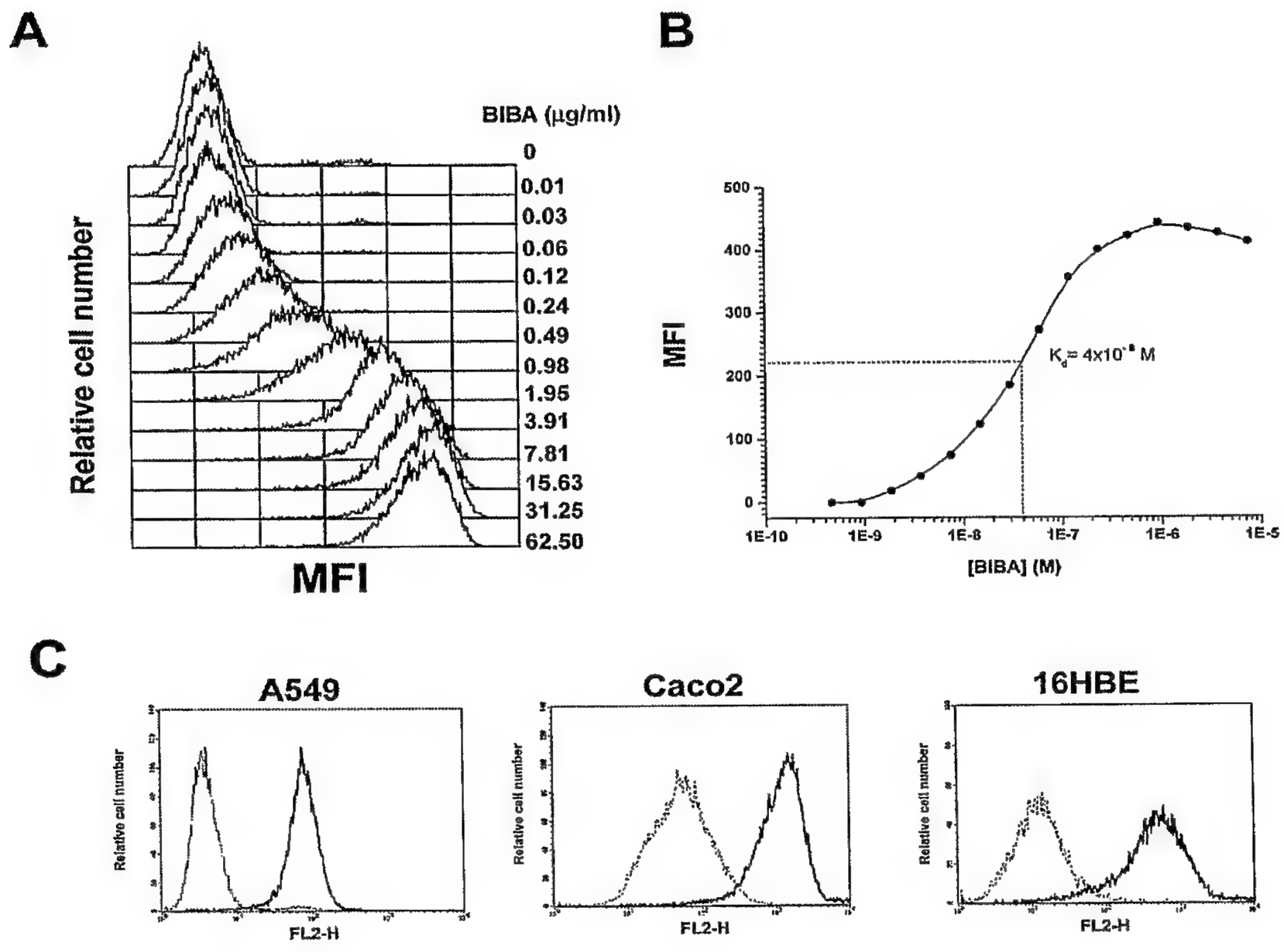
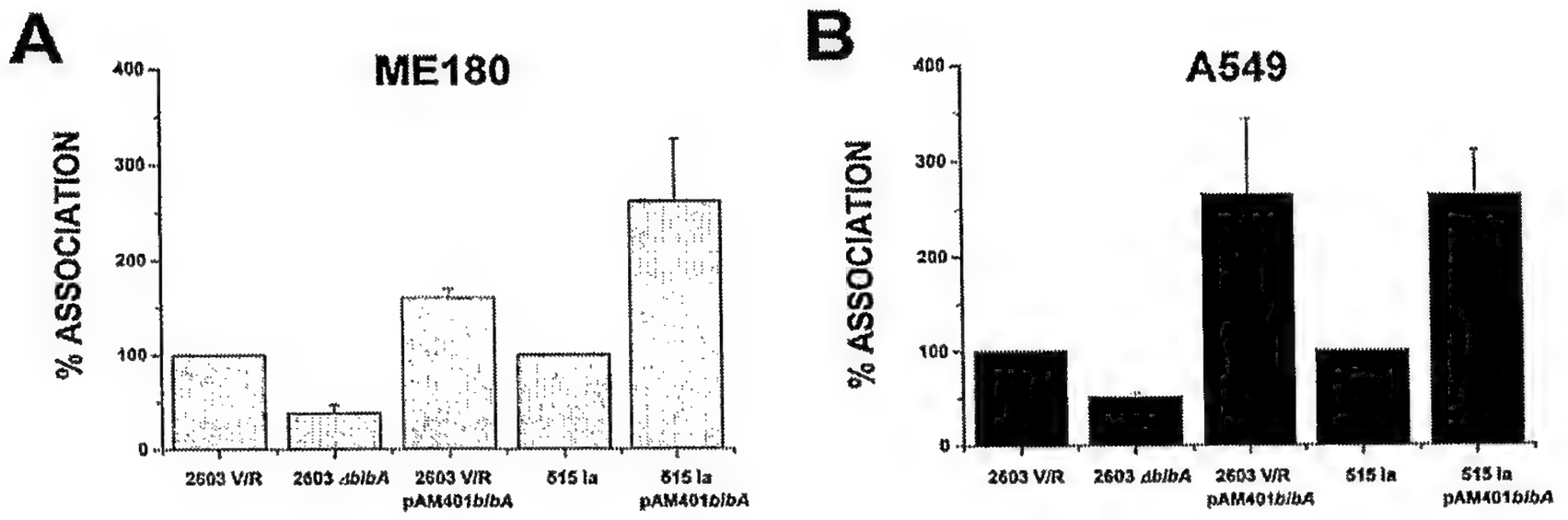

A
BIBA (µg/ml)
0
0.01
0.03
0.06
0.12
0.24
0.49
0.98
1.95
3.91
7.81
15.63
31.25
62.50
Relative cell number
MFI
B
MFI
500
400
300
200
100
0
1E-10
1E-9
1E-8
1E-7
1E-6
1E-5
[BIBA] (M)
C
A549
Caco2
16HBE
Relative cell number
FL2-H

Fig. 23


A
ME180
% ASSOCIATION
400
300
200
100
0
2603 V/R
2603 ΔbibA
2603 V/R pAM401bibA
515 Ia
515 Ia pAM401bibA
B
A549
% ASSOCIATION
400
300
200
100
0
2603 V/R
2603 ΔbibA
2603 V/R pAM401bibA
515 Ia
515 Ia pAM401bibA

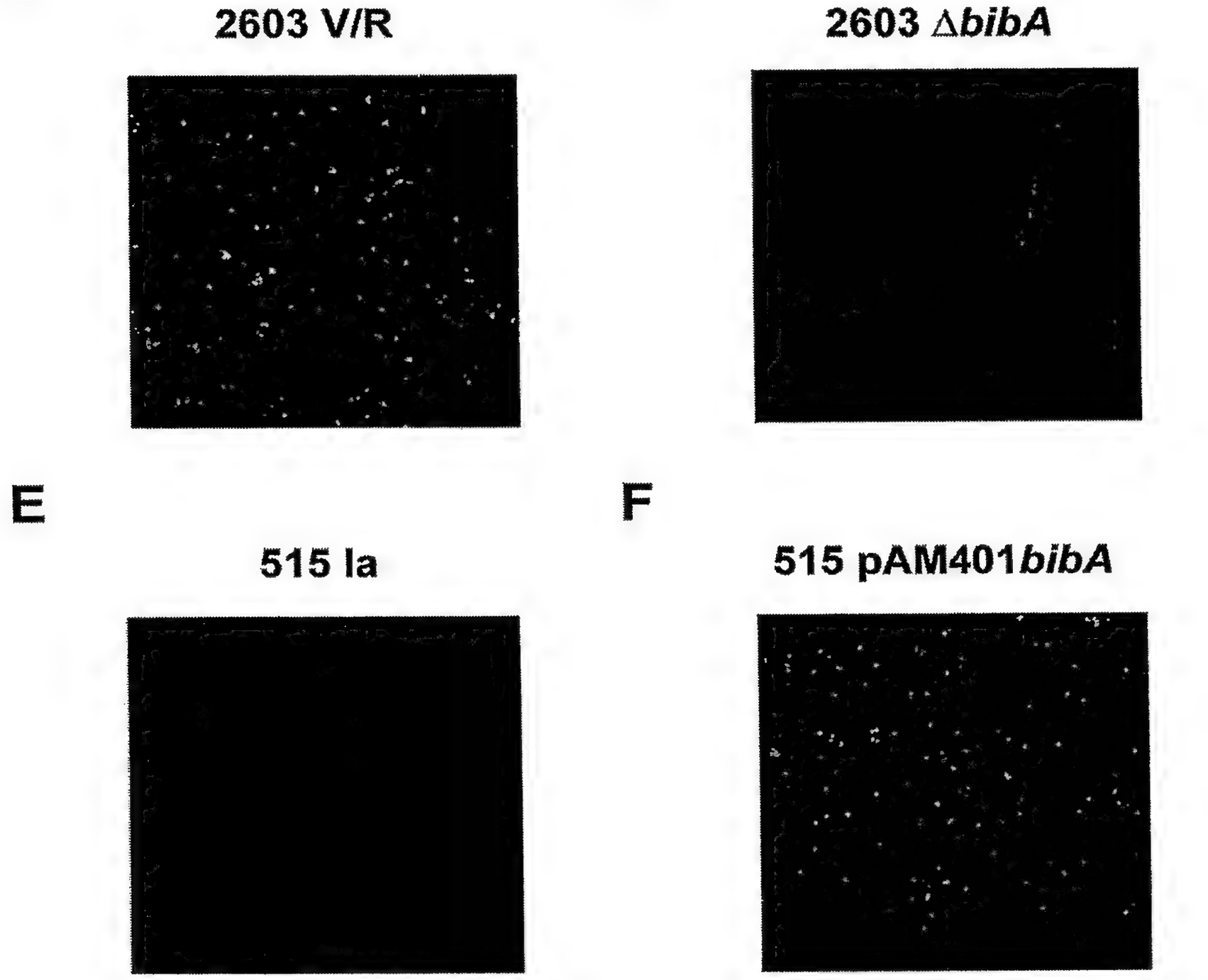

C
2603 V/R
D
2603 ΔbibA
E
515 Ia
F
515 pAM401bibA

Fig. 24

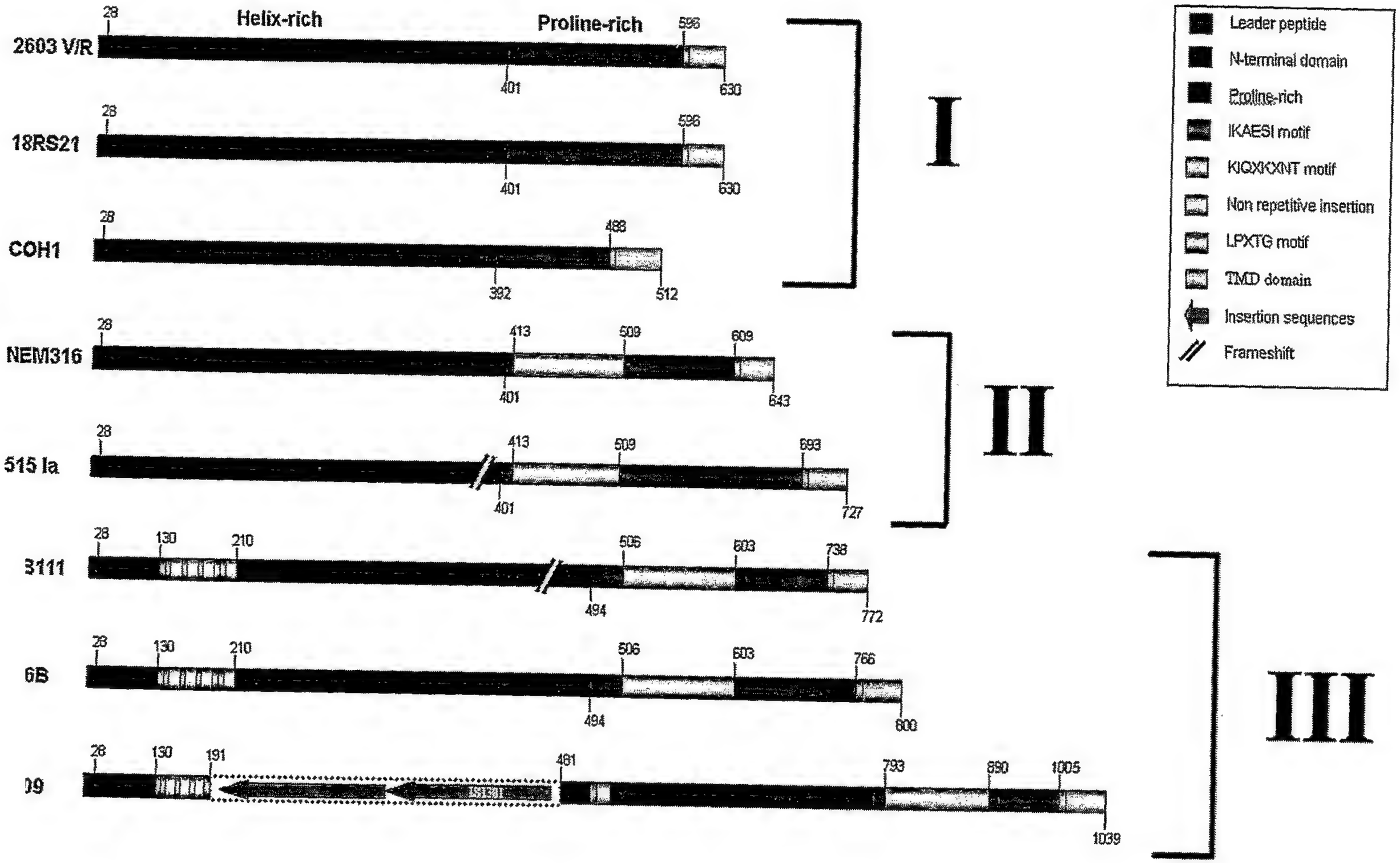
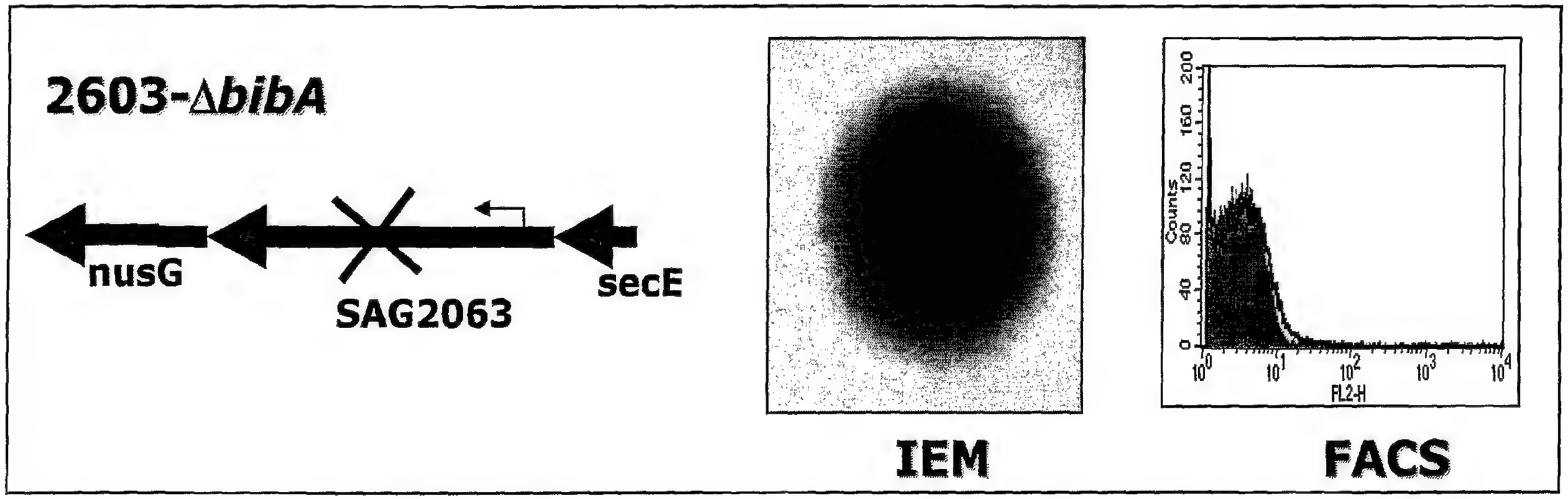

Helix-rich
Proline-rich
2603 V/R
28
401
596
630
18RS21
28
401
596
630
COH1
28
392
488
512
NEM316
28
401
413
509
609
643
515 Ia
28
401
413
509
693
727
3111
28
130
210
494
506
603
738
772
6B
28
130
210
494
506
603
766
800
09
28
130
191
481
793
890
1005
1039
I
II
III
Leader peptide
N-terminal domain
Proline-rich
IKAESI motif
KIQXKXNT motif
Non repetitive insertion
LPXTG motif
TMD domain
Insertion sequences
Frameshift

FIG. 25


2603-ΔbibA
nusG
SAG2063
secE
IEM
Counts
FL2-H
FACS

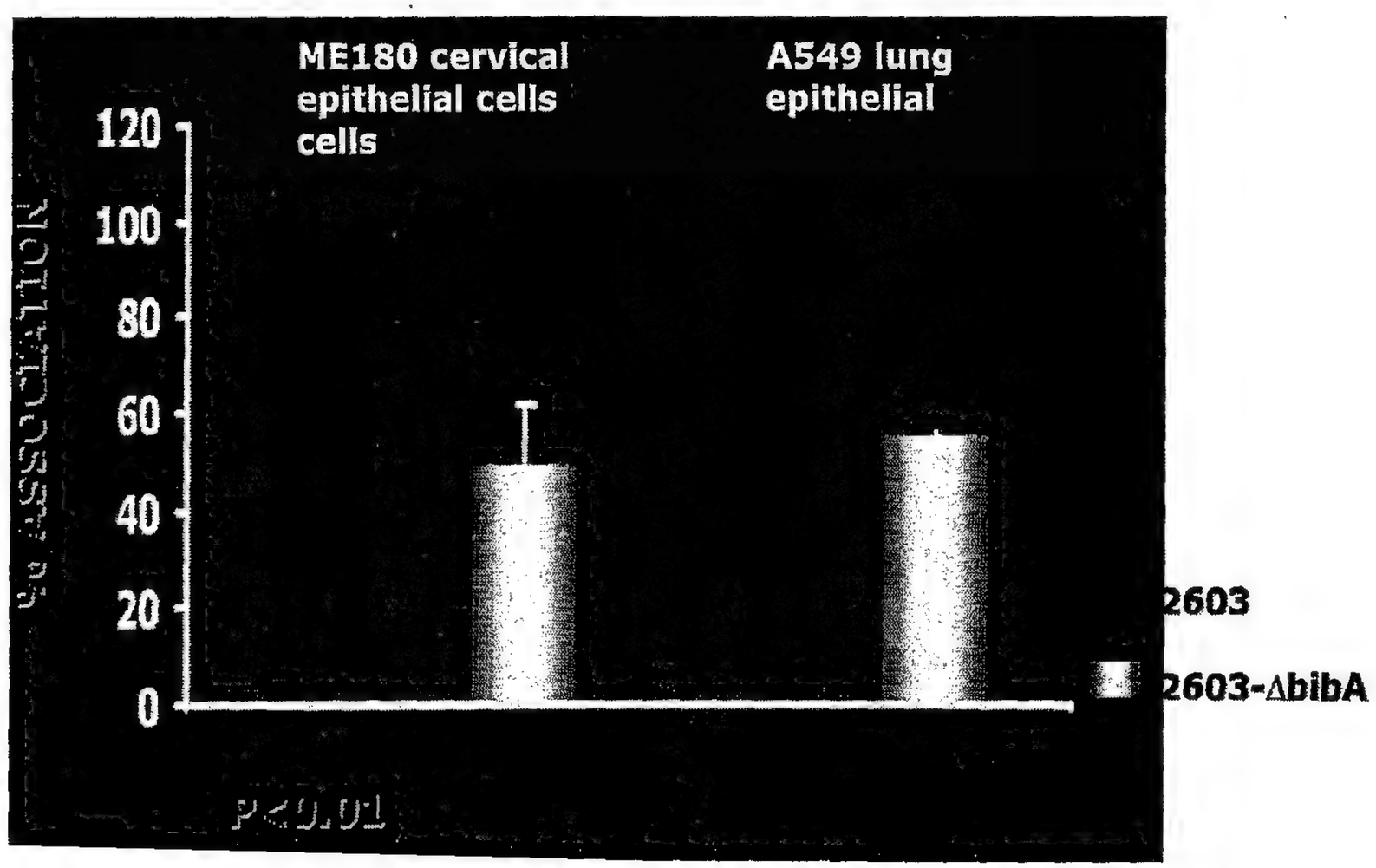
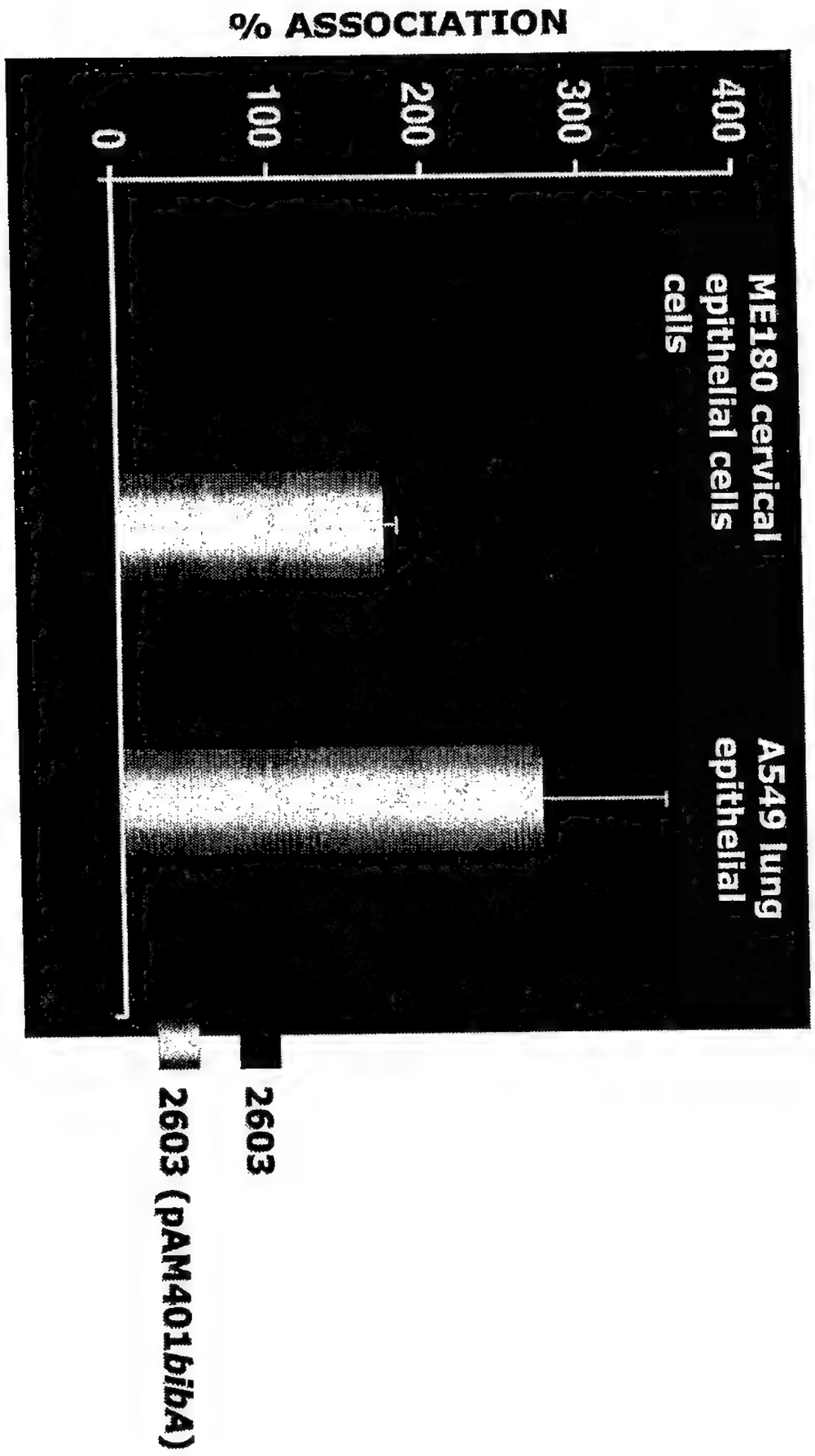
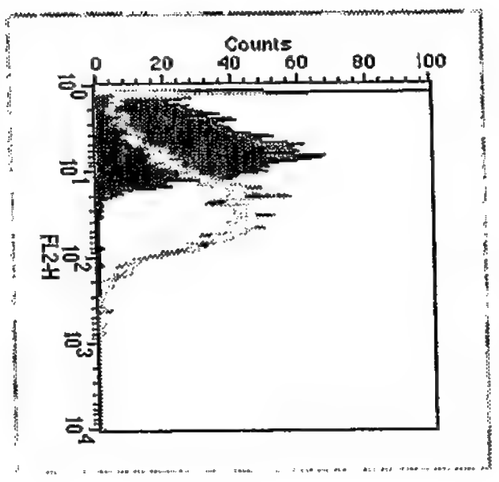

ME180 cervical epithelial cells cells
A549 lung epithelial
% ASSOCIATION
120
100
80
60
40
20
0
2603
2603-ΔbibA
P<0.01

FIG. 26

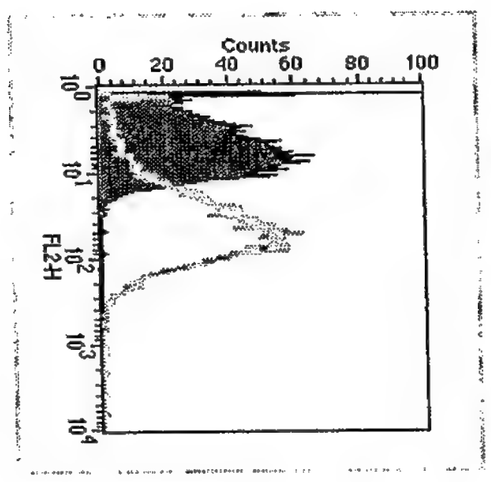


2603 V/R



Δmean=184

2603(pAM401-*bibA*)



Δmean=242

Fig. 27

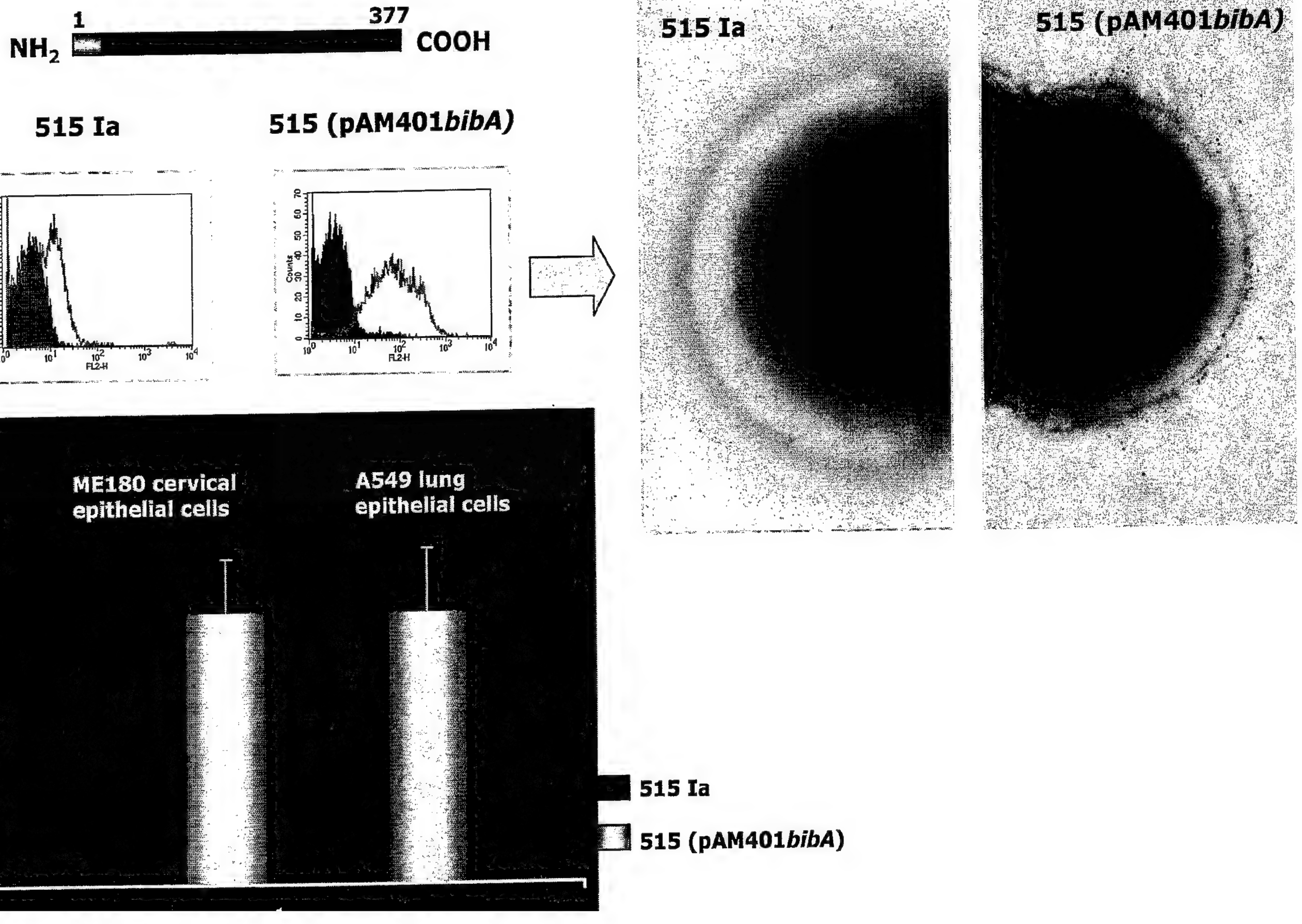
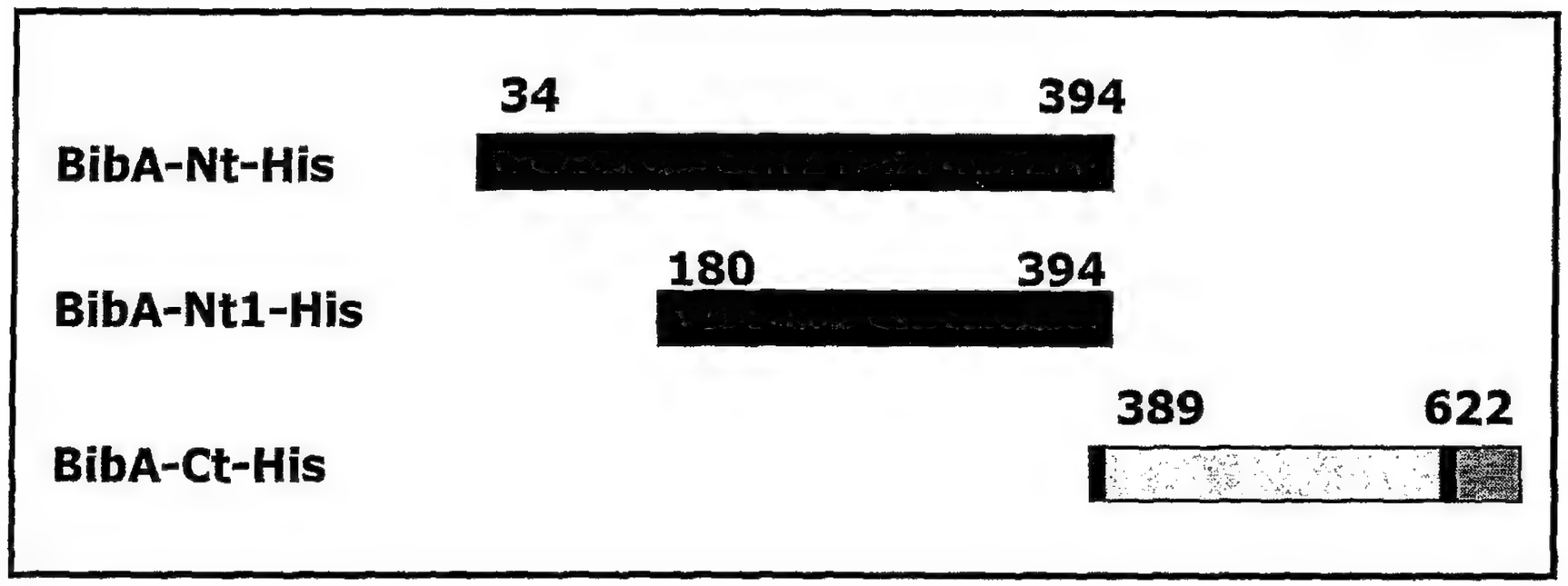
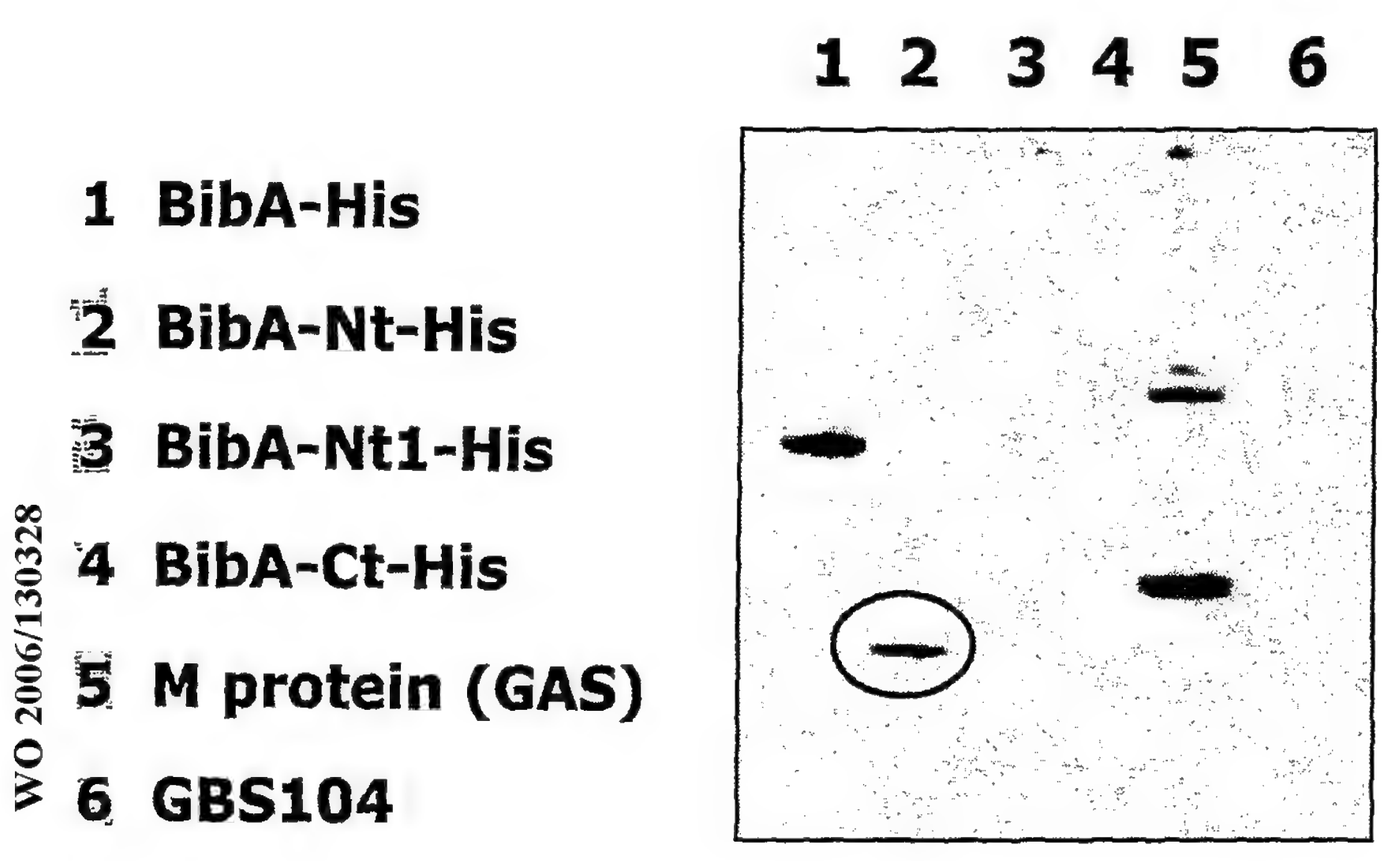

1
377
NH2
COOH
515 Ia
515 (pAM401bibA)
Counts
FL2-H
515 Ia
515 (pAM401bibA)
400
ME180 cervical epithelial cells
A549 lung epithelial cells
515 Ia
515 (pAM401bibA)

Fig. 28


34
394
BibA-Nt-His
180
394
BibA-Nt1-His
389
622
BibA-Ct-His


1 2 3 4 5 6
1 BibA-His
2 BibA-Nt-His
3 BibA-Nt1-His
4 BibA-Ct-His
5 M protein (GAS)
6 GBS104

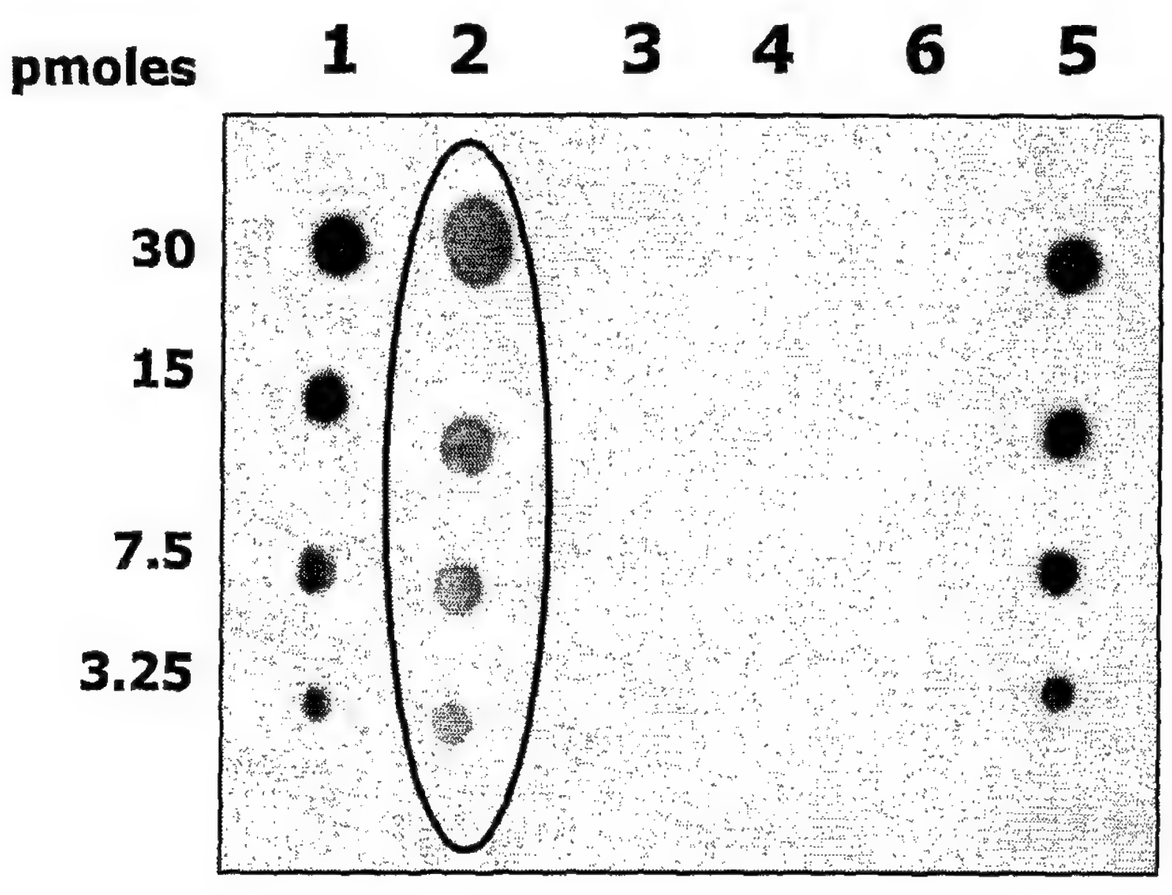
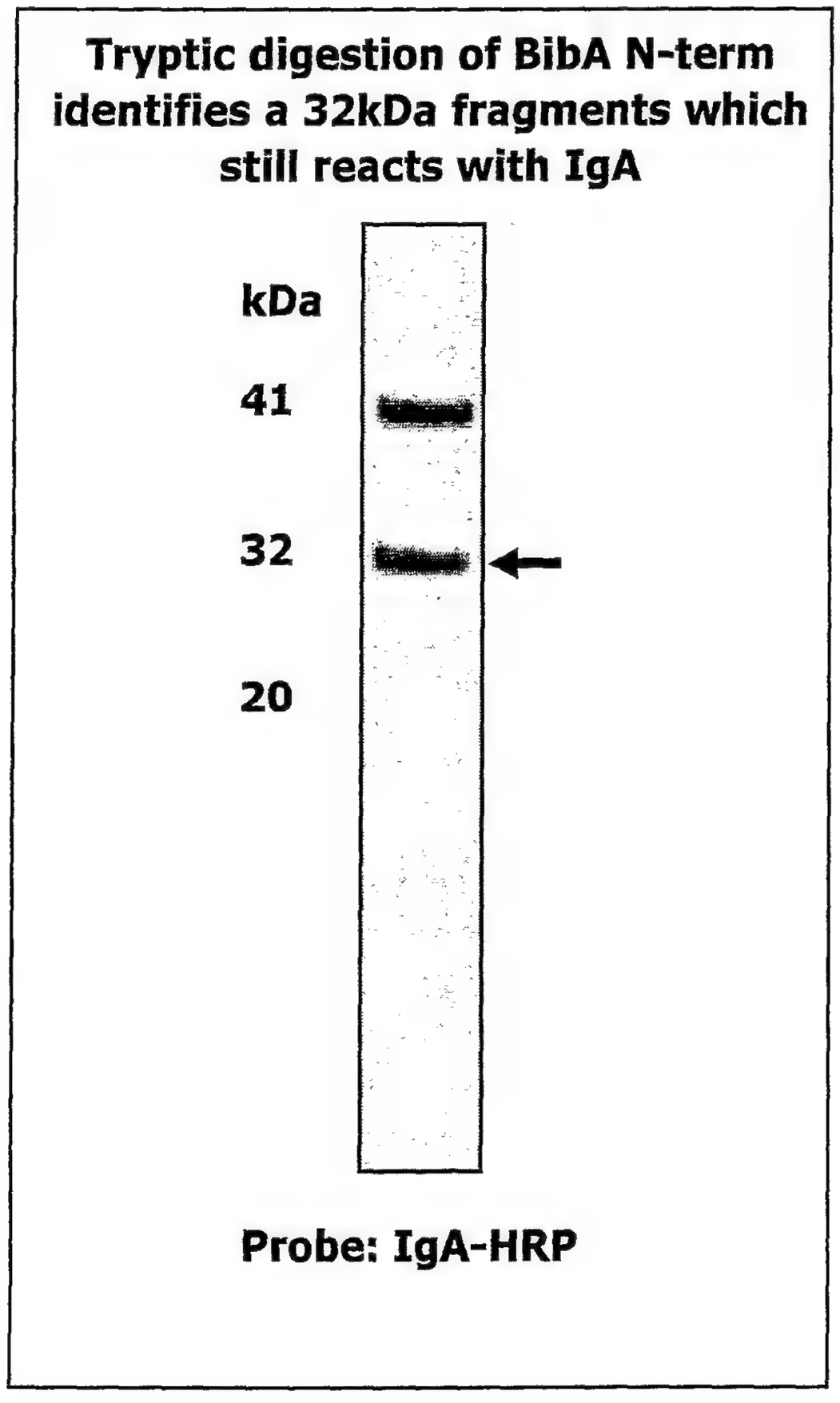

pmoles
1 2 3 4 6 5
30
15
7.5
3.25

Fig. 29


Tryptic digestion of BibA N-term identifies a 32kDa fragments which still reacts with IgA
kDa
41
32
20
Probe: IgA-HRP

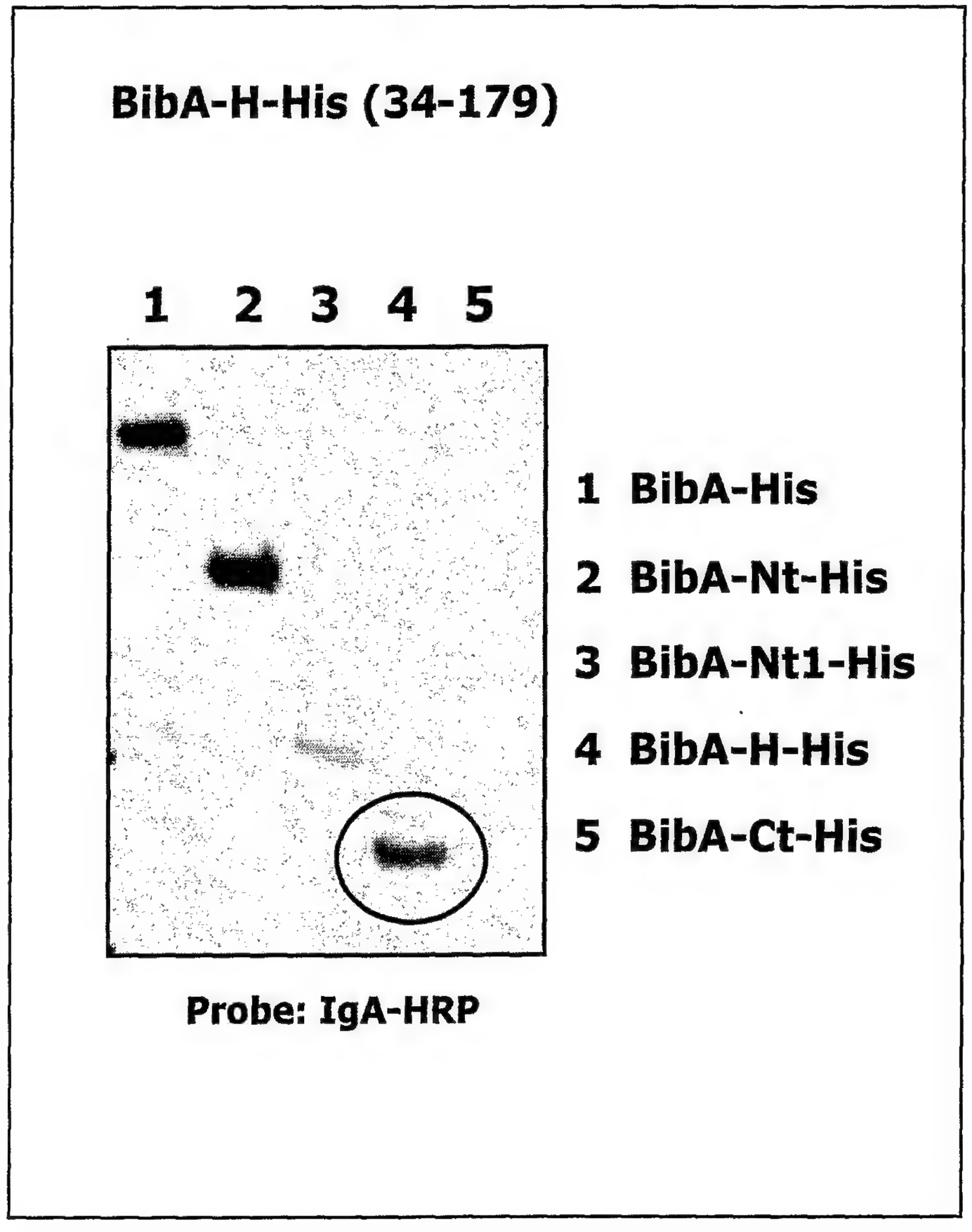
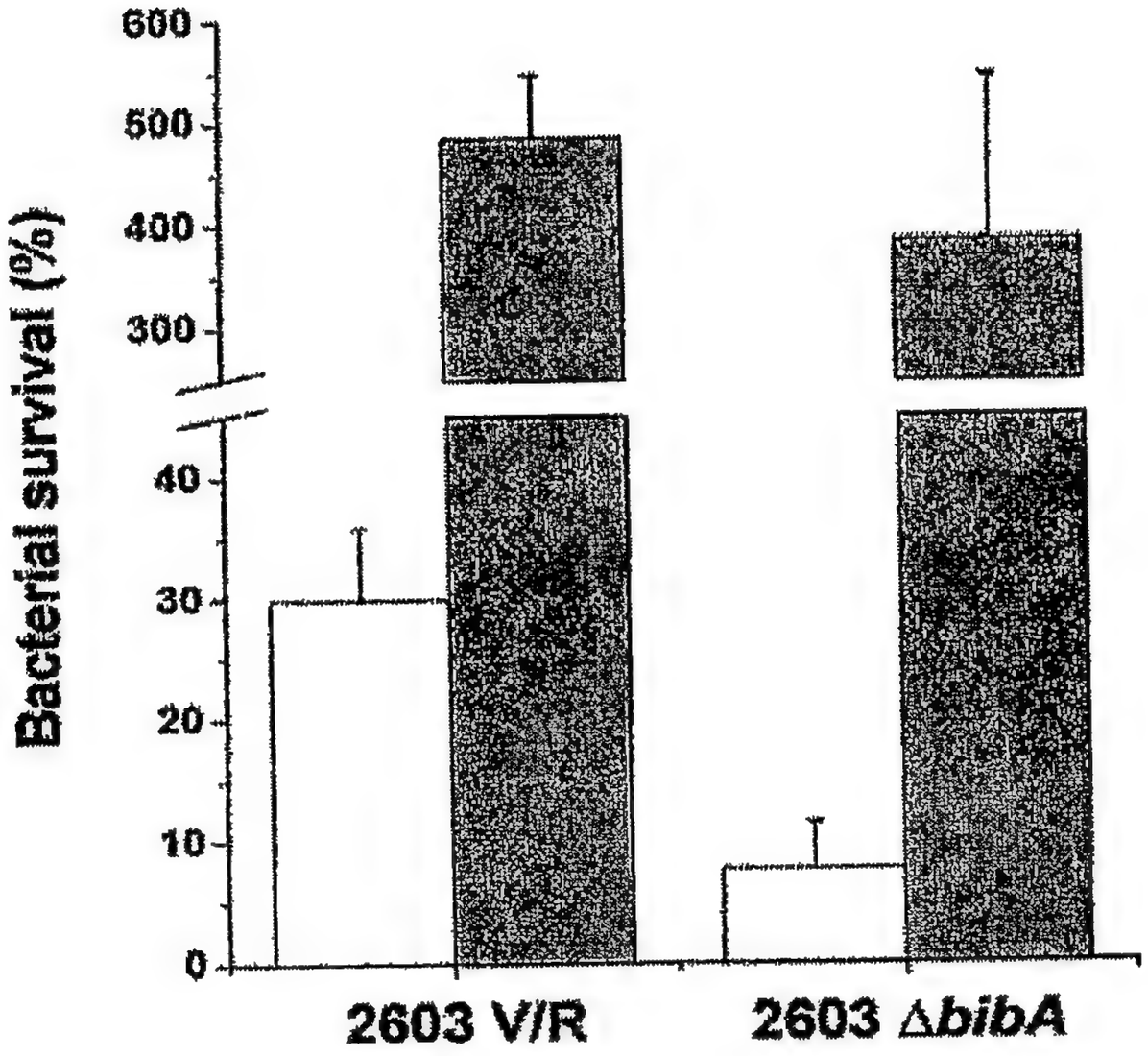

BibA-H-His (34-179)
1 2 3 4 5
1 BibA-His
2 BibA-Nt-His
3 BibA-Nt1-His
4 BibA-H-His
5 BibA-Ct-His
Probe: IgA-HRP

FIG. 30


Bacterial survival (%)
600
500
400
300
40
30
20
10
0
2603 V/R
2603 ΔbibA

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
7 December 2006 (07.12.2006)

PCT

(10) International Publication Number
WO 2006/130328 A3

(51) International Patent Classification:
C07K 14/315 (2006.01)

(21) International Application Number:
PCT/US2006/018411

(22) International Filing Date: 12 May 2006 (12.05.2006)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/680,479 13 May 2005 (13.05.2005) US
60/740,291 29 November 2005 (29.11.2005) US

(71) Applicant *(for all designated States except US)*: **NOVARTIS VACCINES AND DIAGNOSTICS, INC.** [US/US]; 4560 Horton Street, Emeryville, CA 94608 (US).

(72) Inventors; and
(75) Inventors/Applicants *(for US only)*: **SORIANI, Marco** [IT/IT]; Via Fiorentina, 1, I-53100 Siena (IT). **SANTI, Isabella** [IT/IT]; Via Fiorentina, 1, I-53100 Siena (IT).

(74) Common Representative: **NOVARTIS VACCINES AND DIAGNOSTICS, INC.**; 4560 Horton Street, Emeryville, CA 94608 (US).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, LY, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:
— *with international search report*
— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments*

(88) Date of publication of the international search report:
18 May 2007

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 2006/130328 A3

(54) Title: SERUM RESISTANCE FACTORS OF GRAM POSITIVE BACTERIA

(57) Abstract: A newly identified serum resistance factor of gram positive bacteria can be used to treat or prevent bacterial infection.

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2006/018411

A. CLASSIFICATION OF SUBJECT MATTER
INV. C07K14/315

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
EPO-Internal, BIOSIS, MEDLINE, WPI Data, Sequence Search

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 02/34771 A (CHIRON SPA [IT]; INST GENOMIC RES [US]; TELFORD JOHN [IT]; MASIGNANI V) 2 May 2002 (2002-05-02)	24-27
Y	see SEQ ID. Nos 6265, 6266, 8957, 8958, 3874sequences 6265, 6266, 8957, 8958	1-59
X	TETTELIN H ET AL: "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE, WASHINGTON, DC, US, vol. 99, no. 19, 17 September 2002 (2002-09-17), pages 12391-12396, XP002268223 ISSN: 0027-8424	24-27
Y	page 12394; sequence SAG2063	1-59

-/--

[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
14 March 2007	29/03/2007

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL – 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Paresce, Donata

INTERNATIONAL SEARCH REPORT

International application No
PCT/US2006/018411

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	TETTELIN H ET AL: "Complete genome sequence of a virulent isolate of Streptococcus pneumoniae" SCIENCE, AMERICAN ASSOCIATION FOR THE ADVANCEMENT OF SCIENCE,, US, vol. 293, no. 5529, 2001, pages 498-506, XP002218261 ISSN: 0036-8075 page 504 - page 505	1-59
Y	WO 02/092818 A2 (PASTEUR INSTITUT [FR]; CENTRE NAT RECH SCIENT [FR]; GLASER PHILIPPE [F) 21 November 2002 (2002-11-21) claim 6; sequence 2967	1-59
Y	WO 2004/099242 A (INTERCELL AG [AT]; MEINKE ANDREAS [AT]; NAGY ESZTER [AT]; HANNER MARKU) 18 November 2004 (2004-11-18) claim 12; sequence 364	1-59

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2006/018411

Box II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Although claims 35, 56 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

2. [ ] Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. [ ] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

[ ] The additional search fees were accompanied by the applicant's protest.

[ ] No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/US2006/018411

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
WO 0234771	A	02-05-2002	AU	1412702 A	06-05-2002
			CA	2425303 A1	02-05-2002
			EP	1328543 A2	23-07-2003
			MX	PA03003690 A	05-05-2004
			NZ	524888 A	29-09-2006
			US	2006210579 A1	21-09-2006
WO 02092818	A2	21-11-2002	FR	2824074 A1	31-10-2002
WO 2004099242	A	18-11-2004	AU	2004235952 A1	18-11-2004
			CA	2522986 A1	18-11-2004
			US	2006269541 A1	30-11-2006